

Copyright GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 24, 2006, 23:51:43 ; Search time 51 Seconds
(without alignments)

34.326 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 20

Sequence: 1 YGRKVRQRRKPASADGHR 20

Scoring table: Oligo Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 1

Total number of hits satisfying chosen parameters: 641544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents_AA.*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	12	60.0	12	2	US-09-556-121-14	Sequence 14, App1
2	12	60.0	12	2	US-09-656-121-15	Sequence 15, App1
3	11	55.0	11	1	US-08-706-741B-54	Sequence 54, App1
4	11	55.0	11	1	US-08-924-695A-54	Sequence 54, App1
5	11	55.0	11	2	US-09-208-066-2	Sequence 2, App1
6	11	55.0	11	2	US-09-296-089-37	Sequence 37, App1
7	11	55.0	11	2	US-09-837-063-2	Sequence 2, App1
8	11	55.0	11	2	US-09-660-742-1	Sequence 1, App1
9	11	55.0	11	2	US-09-434-345-2	Sequence 2, App1
10	11	55.0	11	2	US-09-632-387A-22	Sequence 22, App1
11	11	55.0	11	2	US-09-632-377A-4	Sequence 4, App1
12	11	55.0	11	2	US-09-612-033B-15	Sequence 15, App1
13	11	55.0	11	2	US-09-780-070-37	Sequence 37, App1
14	11	55.0	11	2	US-09-775-052A-2	Sequence 2, App1
15	11	55.0	11	2	US-09-911-842A-6	Sequence 6, App1
16	11	55.0	11	2	US-09-97-465B-2	Sequence 2, App1
17	11	55.0	11	2	US-10-083-889-17	Sequence 17, App1
18	11	55.0	11	2	US-09-551-976-37	Sequence 37, App1
19	11	55.0	11	2	US-09-265-107-75	Sequence 75, App1
20	11	55.0	11	2	US-09-724-126A-16	Sequence 16, App1
21	11	55.0	11	2	US-09-545-433-14	Sequence 14, App1
22	11	55.0	11	2	US-10-031-505-12	Sequence 12, App1
23	11	55.0	11	2	US-10-144-549-6	Sequence 6, App1
24	11	55.0	11	2	US-09-825-414-91	Sequence 91, App1
25	11	55.0	11	2	US-10-286-596-22	Sequence 22, App1
26	11	55.0	11	2	US-09-909-474D-5	Sequence 5, App1

ALIGNMENTS

RESULT 1
US-09-656-121-14
; Sequence 14, Application US/09656121
; Patent No. 6706892
; GENERAL INFORMATION:
; APPLICANT: CONJUCHEM, INC.
; APPLICANT: EBRIN, ALAN M.
; APPLICANT: FLESER, ANGELICA
; APPLICANT: ROBITAILLE, MARTIN
; APPLICANT: MILNER, PETER G.
; APPLICANT: BRIDON, DOMINIQUE P.
; TITLE OF INVENTION: PULMONARY DELIVERY FOR BIOCONJUGATION
; CURRENT APPLICATION NUMBER: US/09/656,121
; CURRENT FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/152,681
; PRIOR FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-656-121-14
Query Match Score 60.0%; Best Local Similarity 100.0%; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YGRKVRQRRRK 12
Db 1 YGRKVRQRRRK 12

RESULT 2
US-09-656-121-15
; Sequence 15, Application US/09656121
; Patent No. 6706892
; GENERAL INFORMATION:
; APPLICANT: CONJUCHEM, INC.
; APPLICANT: EBRIN, ALAN M.
; APPLICANT: FLESER, ANGELICA
; APPLICANT: ROBITAILLE, MARTIN
; APPLICANT: MILNER, PETER G.
; APPLICANT: BRIDON, DOMINIQUE P.
; TITLE OF INVENTION: PULMONARY DELIVERY FOR BIOCONJUGATION

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FILE REFERENCE: REDC-1810
CURRENT APPLICATION NUMBER: US/09/6556,121
CURRENT FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/152,681
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 15
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-6556-121-15

Query Match      60.0%; Score 12; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 YGRKKRRQRRK 12
Db    1 YGRKKRRQRRK 12

RESULT 3
US-08-706-741B-54
Sequence 54, Application US/08706741B
Patent No. 5955593
GENERAL INFORMATION:
APPLICANT: KORMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63146

COMPUTER READABLE FORM:
SEQUENCE FORMATTED AS A PROTEIN:
MEDIAN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,741B
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971798
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6992
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-924-695A-54

Query Match      55.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 YGRKKRRQRR 11
Db    1 YGRKKRRQRR 11

RESULT 4
US-08-924-695A-54
Sequence 54, Application US/08924695A
Patent No. 5998883
GENERAL INFORMATION:
APPLICANT: KORMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105

COMPUTER READABLE FORM:
SEQUENCE FORMATTED AS A PROTEIN:
MEDIAN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,695A
FILING DATE: 09-SEP-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971798
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6992
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-924-695A-54

Query Match      55.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 YGRKKRRQRR 11
Db    1 YGRKKRRQRR 11

RESULT 5
US-09-208-966-2
Sequence 2, Application US/09208966
Patent No. 6221355
GENERAL INFORMATION:
APPLICANT: Dowdy, Steven F.
TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
FILE REFERENCE: 48881/1742
CURRENT APPLICATION NUMBER: US/09/208,966
CURRENT FILING DATE: 1998-12-10
EARLIER APPLICATION NUMBER: 60/082,402
EARLIER FILING DATE: 1998-04-20
EARLIER APPLICATION NUMBER: 60/059,012
EARLIER FILING DATE: 1997-12-10
NUMBER OF SEQ ID NOS: 57
SEQ ID NO 2
LENGTH: 11
TYPE: PRT
ORGANISM: human
US-09-208-966-2

Query Match      55.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 YGRKKRRQRR 11
Db    1 YGRKKRRQRR 11

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Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0; Organism: Human immunodeficiency virus

Query 1 YGRKRRQRRR 11
Database 1 YGRKRRQRRR 11

RESULT 6
US-09-296-089-37
Sequence 37, Application US/09296089
General Information:
Applicant: Blaschuk, Orest W.
Applicant: Byers, Stephen
Title of Invention: COMPOUNDS AND METHODS FOR MODULATING TITLE OF INVENTION: BETA-CATENIN MEDIATED GENE EXPRESSION
File Reference: 100086_411
Current Application Number: US/09/296.089
Current Filing Date: 1999-04-21
Number of SEQ ID NOS: 37
Software: FastSEQ for Windows Version 3.0
SEQ ID NO 37
Length: 11
Type: PRT
Organism: Human immunodeficiency virus

US-09-296-089-37

Query Match 55.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
US-09-434-345-2
Sequence 2, Application US/09434345
General Information:
Applicant: Boulikas, Teni
Title of Invention: THERAPY FOR HUMAN CANCERS USING CISPLATIN AND OTHER DRUGS OR GENES ENCAPSULATED INTO LIPOSOMES
File Reference: TB 2001-00
Current Application Number: US/09/434,345
General Information:
Title of Invention: CISPLATIN AND OTHER DRUGS OR GENES ENCAPSULATED INTO LIPOSOMES
File Reference: TB 2001-00
Current Application Number: US/09/434,345
Number of SEQ ID NOS: 10
Software: FastSEQ for Windows Version 4.0
SEQ ID NO 2
Length: 11
Type: PRT
Organism: Human Immunodeficiency Virus

US-09-434-345-2

Query Match 55.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
US-09-632-287A-22
Sequence 22, Application US/09632287A
General Information:
Applicant: Hsu, Hailing
Title of Invention: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
File Reference: 01017/3550A
Current Application Number: US/09/632,287A
Current Filing Date: 2000-08-03
Prior Application Number: US 60/147,294
Prior Filing Date: 1999-08-04

US-09-632-287A-22

Query Match 55.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
US-09-660-742-1

Query Match 55.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
US-09-837-863-2
Sequence 2, Application US/09837863
General Information:
Applicant: Greene, Amy
Applicant: Zhou, Hua
Applicant: Thode, Silke
Title of Invention: Vector and Method for Targeted Replacement and Disruption of an Integrated DNA Sequence
File Reference: 025.JUS
Current Application Number: US/09/837,863
Current Filing Date: 2001-04-17
Prior Application Number: US 60/198,498
Prior Filing Date: 2000-04-18
Number of SEQ ID NOS: 27
Software: PatentIn version 3.0
SEQ ID NO 2
Type: PRT
Organism: Human immunodeficiency virus

US-09-837-863-2

Query Match 55.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;

NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 22
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Peptide from the HIV TAT protein
 US-09-632-287A-22

Query Match 55.0%; Score 11; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
 Db 1 YGRKKRQRRR 11

RESULT 13
 US-09-780-070-37
 Sequence 37, Application US/09780070
 / Patent No. 6632656
 / GENERAL INFORMATION:
 / APPLICANT: Burke, James
 / APPLICANT: Strittmayer, Warren
 / APPLICANT: Nagai, Yoshitaka
 / TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT
 / TITLE OF INVENTION: AND METHODS OF USE THEREOF
 / FILE REFERENCE: 5405_242
 / CURRENT APPLICATION NUMBER: US/09/780,070
 / CURRENT FILING DATE: 2003-02-09
 / PRIOR APPLICATION NUMBER: 60/189,781
 / PRIOR FILING DATE: 2000-03-16
 / NUMBER OF SEQ ID NOS: 40
 / SOFTWARE: PatentIn version 3.0
 / SEQ ID NO 37
 / LENGTH: 11
 / TYPE: PRT
 / ORGANISM: Human immunodeficiency virus
 US-09-780-070-37

Query Match 55.0%; Score 11; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
 Db 1 YGRKKRQRRR 11

RESULT 14
 US-09-775-052A-2
 Sequence 2, Application US/09775052A
 / Patent No. 6645501
 / GENERAL INFORMATION:
 / APPLICANT: Dowdy, Steven F.
 / TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
 / FILE REFERENCE: 48881/1742
 / CURRENT APPLICATION NUMBER: US/09/775,052A
 / CURRENT FILING DATE: 2001-12-05
 / PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966
 / PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
 / PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,012
 / PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10
 / NUMBER OF SEQ ID NOS: 57
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 2
 / LENGTH: 11
 / TYPE: PRT
 / ORGANISM: human
 US-09-775-052A-2

Query Match 55.0%; Score 11; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
 Db 1 YGRKKRQRRR 11

RESULT 12
 US-09-612-031B-15
 Sequence 15, Application US/09612033B
 / Patent No. 6627199
 / GENERAL INFORMATION:
 / APPLICANT: Saris, Chris
 / TITLE OF INVENTION: Isolation, Identification, and Characterization of a Member of the TNF-Receptor Superfamily
 / TITLE OF INVENTION: tmst2, a No. 6627199el Member of the TNF-Receptor Superfamily
 / FILE REFERENCE: 01017/35434A
 / CURRENT APPLICATION NUMBER: US/09/612,033B
 / CURRENT FILING DATE: 2000-07-07
 / PRIOR APPLICATION NUMBER: US 60/143,063
 / PRIOR FILING DATE: 1999-07-09
 / NUMBER OF SEQ ID NOS: 15
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 15
 / LENGTH: 11
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: peptide
 US-09-612-033B-15

RESULT 15
US-09-911-842A-6
Sequence 6, Application US/09911842A
Patent No. 6656707
GENERAL INFORMATION:
APPLICANT: Angen Inc.
FILE REFERENCE: 01017137592
TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/911,842A
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: US 60/222,438
PRIOR FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-911-842A-6

Query Match 55.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy YGRKGRQR 11
| || || | | | |
Db YGRKGRQR 11

Search completed: August 24, 2006, 23:53:08
Job time : 52 secs

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Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	5 US-10-814-109-2	Sequence 2, Appli
2	12	60.0	12	4 US-10-756-774-14	Sequence 14, Appli
3	4	12	60.0	12	4 US-10-756-774-15
4	12	60.0	20	5 US-10-930-192-4	Sequence 4, Appli
5	12	60.0	20	5 US-10-930-192-5	Sequence 5, Appli
6	12	60.0	20	5 US-10-930-192-12	Sequence 12, Appli
7	60.0	20	6	US-11-021-928A-276	Sequence 276, Appli
8	12	60.0	20	6 US-11-021-928A-363	Sequence 363, Appli
9	12	60.0	20	6 US-11-021-928A-364	Sequence 364, Appli
10	12	60.0	22	3 US-09-949-196-22	Sequence 22, Appli
11	12	60.0	22	3 US-09-949-196-34	Sequence 34, Appli
12	11	55.0	11	3 US-09-779-791A-1	Sequence 1, Appli
13	11	55.0	11	3 US-09-825-414-91	Sequence 37, Appli
14	11	55.0	11	3 US-09-815-108-9	Sequence 9, Appli
15	11	55.0	11	3 US-09-886-404-13	Sequence 13, Appli
16	11	55.0	11	3 US-09-805-805-8	Sequence 8, Appli
17	11	55.0	11	3 US-09-821-821-24	Sequence 24, Appli
18	11	55.0	11	3 US-09-895-941-13	Sequence 13, Appli
19	11	55.0	11	3 US-09-925-414-91	Sequence 91, Appli
20	11	55.0	11	3 US-09-867-274-23	Sequence 23, Appli
21	11	55.0	11	3 US-09-955-866-24	Sequence 24, Appli
22	11	55.0	11	3 US-09-928-175-25	Sequence 25, Appli
23	11	55.0	11	3 US-09-995-542-13	Sequence 13, Appli
24	11	55.0	11	3 US-09-927-851-18	Sequence 13, Appli
25	11	55.0	11	3 US-09-884-103-4	Sequence 4, Appli
26	11	55.0	11	3 US-09-949-186-15	Sequence 15, Appli
27	11	55.0	11	3 US-09-948-018-22	Sequence 22, Appli

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; TYPE: PRT ; OTHER INFORMATION: synthetic peptide
; ORGANISM: Artificial Sequence ; US-10-930-192-4
; FEATURE: Synthetic Peptide
; OTHER INFORMATION: Synthetic Peptide
US-10-756-774-14

Query Match Score 12; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0001; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRRK 12
Db 1 YGRKERRQRRRK 12

RESULT 5
US-10-930-192-5
; Sequence 5, Application US/10930192
; Publication No. US2005005959/A1
; GENERAL INFORMATION:
; APPLICANT: Tymianski, Michael
; TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells
; FILE REFERENCE: 4438 0007
; CURRENT APPLICATION NUMBER: US/10/930.192
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: US 10/208,374
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/584,555
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-930-192-5

Query Match Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00015; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRRK 12
Db 1 YGRKERRQRRRK 12

RESULT 6
US-10-930-192-12
; Sequence 12, Application US/10930192
; Publication No. US2005005959/A1
; GENERAL INFORMATION:
; APPLICANT: Tymianski, Michael
; TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells
; FILE REFERENCE: 4438 0007
; CURRENT APPLICATION NUMBER: US/10/930.192
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: US 10/208,374
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/584,555
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-930-192-12

Query Match Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00015; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRRK 12
Db 1 YGRKERRQRRRK 12

RESULT 4
US-10-930-192-4
; Sequence 4, Application US/10930192
; Publication No. US2005005959/A1
; GENERAL INFORMATION:
; APPLICANT: Tymianski, Michael
; TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells
; FILE REFERENCE: 4438 0007
; CURRENT APPLICATION NUMBER: US/10/930.192
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: US 10/208,374
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/584,555
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-930-192-12

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GENERAL INFORMATION:

APPLICANT: Tymianski, Michael
 TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells
 FILE REFERENCE: 1889-00800
 CURRENT APPLICATION NUMBER: US/11/021,928A
 CURRENT FILING DATE: 2004-12-22
 PRIOR FILING DATE: 2004-12-22
 NUMBER OF SEQ ID NOS: 384
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 364
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic peptide

US-11-021-928A-364

Query Match Score 60.0%; Pred. No. 0.00015; Length 20;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Number of SEQ ID NOS: 384
 SEQ ID NO: 276
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic peptide

US-11-021-928A-276

Query Match Score 60.0%; Pred. No. 0.00015; Length 20;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Number of SEQ ID NOS: 384
 SEQ ID NO: 12
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic peptide

RESULT 7

US-11-021-928A-276

Sequence 276, Application US/11021928A
 Publication No. US20050164933A1

GENERAL INFORMATION:

APPLICANT: Tymianski, Michael
 TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells
 FILE REFERENCE: 1889-00800
 CURRENT APPLICATION NUMBER: US/11/021,928A
 CURRENT FILING DATE: 2004-12-22
 PRIOR FILING DATE: 2004-12-22
 NUMBER OF SEQ ID NOS: 384
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 364
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic peptide

US-11-021-928A-364

Query Match Score 60.0%; Pred. No. 0.00015; Length 20;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Number of SEQ ID NOS: 384
 SEQ ID NO: 12
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic peptide

RESULT 8

US-11-021-928A-363

Sequence 363, Application US/11021928A
 Publication No. US20050164933A1

GENERAL INFORMATION:

APPLICANT: Tymianski, Michael
 TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells
 FILE REFERENCE: 1889-00800
 CURRENT APPLICATION NUMBER: US/11/021,928A
 CURRENT FILING DATE: 2004-12-22
 PRIOR FILING DATE: 2004-12-22
 NUMBER OF SEQ ID NOS: 384
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 363
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic peptide

US-11-021-928A-363

Query Match Score 60.0%; Pred. No. 0.00015; Length 20;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Number of SEQ ID NOS: 384
 SEQ ID NO: 12
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic peptide

RESULT 9

US-11-021-928A-364

Sequence 364, Application US/11021928A
 Publication No. US20050164933A1

GENERAL INFORMATION:

APPLICANT: Tymianski, Michael
 TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells
 FILE REFERENCE: 1889-00800
 CURRENT APPLICATION NUMBER: US/11/021,928A
 CURRENT FILING DATE: 2004-12-22
 PRIOR FILING DATE: 2004-12-22
 NUMBER OF SEQ ID NOS: 384
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 364
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic peptide

US-11-021-928A-364

Query Match Score 60.0%; Pred. No. 0.00015; Length 20;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Number of SEQ ID NOS: 384
 SEQ ID NO: 12
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic peptide

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; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 34
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence
; FEATURE: NAME/KEY: BINDING
; LOCATION: (22)..(22)
; OTHER INFORMATION: NH2
US-09-949-156-34

Query Match          60.0%; Score 12; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
RESULT 14
US-09-815-108-9
; Sequence 9, Application US/09815108
; Patent No. US20020009776A1
; GENERAL INFORMATION:
; APPLICANT: Saris, Christian M.
; APPLICANT: Sharon, Mu X.
; APPLICANT: Xia, Min
; APPLICANT: Boone, Thomas Charles
; APPLICANT: Covey, Todd
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 99-513-A
; CURRENT APPLICATION NUMBER: US/09/815,108
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,379
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-815-108-9

Query Match          55.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00086; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
RESULT 15
US-09-886-404-13
; Sequence 13, Application US/09886404
; Patent No. US20020037524A1
; GENERAL INFORMATION:
; APPLICANT: Medilock, Eugene
; APPLICANT: Yeh, Richard
; APPLICANT: Sibbiger, Scott M.
; APPLICANT: Elliot, Gary S.
; APPLICANT: Nguyen, Hung Q.
; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/37128B
; CURRENT APPLICATION NUMBER: US/09/886,404
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/810,384
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/266,159
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,125
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0

Query Match          55.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00086; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
RESULT 13
US-09-970-070-37
; Sequence 37, Application US/09780070
; Patent No. US200200752A1
; GENERAL INFORMATION:
; APPLICANT: Burke, James
; APPLICANT: Strittmatter, Warren
; APPLICANT: Nagai, Yoshitaka
; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 5405-242
; CURRENT APPLICATION NUMBER: US/09/780,070
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/189,781
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40

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; SEQ ID NO:13
; LENGTH: 11
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Peptide of HIV
; OTHER INFORMATION: TAT protein
; OTHER INFORMATION: US-09-886-404-13
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Query Match      55.00;  Score 11;  DB 3;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 0.00086;
Matches 11;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Qy   1 YGRKKRKRRR 11
     ||||| | |
Db   1 YGRKKRKRRR 11
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Job time : 183 secs
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OM protein - protein search, using SW model

Run on: August 24, 2006, 23:53:23 ; Search time 32 Seconds
(without alignments)
42.764 Million cell updates/sec

Title: US-10-814-109-2
Perfect score: 20
Sequence: 1 YGRKRRQRRKPASADGHR 20

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 247503 seqs, 68422524 residues

Word size : 1

Total number of hits satisfying chosen parameters: 247180

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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- 2: /EMC_Celerra_SIDS3/prodata/1/pubpaas/US06_NEW_PUB.pep;*
- 3: /EMC_Celerra_SIDS3/prodata/1/pubpaas/US07_NEW_PUB.pep;*
- 4: /EMC_Celerra_SIDS3/prodata/1/pubpaas/US08_NEW_PUB.pep;*
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- 7: /EMC_Celerra_SIDS3/prodata/1/pubpaas/US11_NEW_PUB.pep;*
- 8: /EMC_Celerra_SIDS3/prodata/1/pubpaas/US60_NEW_PUB.pep;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	11	55.0	11	6	US-10-547-530-78	Sequence 78, Appli
2	11	55.0	11	6	US-10-547-530-78	Sequence 4, Appli
3	11	55.0	11	6	US-10-547-530-78	Sequence 1, Appli
4	11	55.0	11	7	US-11-318-535-24	Sequence 24, Appli
5	11	55.0	11	7	US-11-318-535-24	Sequence 45, Appli
6	11	55.0	11	7	US-11-318-535-24	Sequence 8, Appli
7	11	55.0	11	7	US-11-318-535-24	Sequence 19, Appli
8	11	55.0	11	7	US-11-318-535-24	Sequence 59, Appli
9	11	55.0	11	7	US-11-318-535-24	Sequence 85, Appli
10	11	55.0	11	7	US-11-318-535-24	Sequence 39, Appli
11	11	55.0	11	7	US-11-318-535-24	Sequence 1, Appli
12	11	55.0	11	7	US-11-318-535-24	Sequence 16, Appli
13	11	55.0	12	7	US-11-318-535-24	Sequence 19, Appli
14	11	55.0	14	7	US-11-318-535-24	Sequence 4, Appli
15	11	55.0	14	7	US-11-318-535-24	Sequence 7, Appli
16	11	55.0	14	7	US-11-318-535-24	Sequence 8, Appli
17	11	55.0	15	7	US-11-318-535-24	Sequence 7, Appli
18	11	55.0	15	7	US-11-318-535-24	Sequence 40, Appli
19	11	55.0	15	7	US-11-318-535-24	Sequence 19, Appli
20	11	55.0	15	7	US-11-318-535-24	Sequence 17, Appli
21	11	55.0	20	6	US-10-539-677-34	Sequence 34, Appli
22	11	55.0	20	6	US-10-539-677-34	Sequence 36, Appli
23	11	55.0	23	7	US-11-251-734-4	Sequence 1, Appli
24	11	55.0	29	7	US-11-251-734-4	Sequence 4, Appli
25	11	55.0	34	7	US-11-251-734-4	Sequence 46, Appli

ALIGNMENTS

RESULT 1
US-10-547-530-78
; Sequence 78, Application US-10-547-530-78
; Publication No. US20060148086A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of California, The
; Leonard, Rome H.
; APPLICANT: Valerie, Kickhoefer A.
; APPLICANT: Phoebe, Raval-Fernandes
; TITLE OF INVENTION: Vault and vault-like Carrier Molecules
; FILE REFERENCE: 143 99-1EP
; CURRENT APPLICATION NUMBER: US-10-547-530-78
; CURRENT FILING DATE: 2005-08-31
; PRIORITY APPLICATION NUMBER: 60/453,800
; PRIORITY FILING DATE: 2003-03-10
; PRIORITY APPLICATION NUMBER: PCT/US04/07434
; PRIORITY FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 78
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-547-530-78

Query Match 55.0%; Score 11; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRKRRQRRR 11
Db 1 YGRKRRQRRR 11
RESULT 2
US-10-518-710-4
; Sequence 4, Application US-10518710
; GENERAL INFORMATION:
; APPLICANT: Tomikawa, Kazuhito
; APPLICANT: Matsui, Hideki
; TITLE OF INVENTION: Inhibitor of constitutive active forming of carcineurin
; FILE REFERENCE: JP-161650
; CURRENT APPLICATION NUMBER: 2004-12-22
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 4

LENGTH: 11
 TYPE: PRT
 ORGANISM: HIV virus
 US-10-518-710-4
 Query Match 55.0%; Score 11; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 APPLICANT: Mizelewski, Gerald J.
 TITLE OF INVENTION: Compositions and Methods of Using Alpha-Peprotein Growth
 FILE REFERENCE: HOLLAND-0516
 CURRENT APPLICATION NUMBER: US/11/223,610
 CURRENT FILING DATE: 2005-09-09
 NUMBER OF SEQ ID NOS: 181
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 45
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-223-610-45

Query Match 55.0%; Score 11; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YGRKKRKQRRL 11
 Db 1 YGRKKRKQRRL 11

RESULT 6
 US-11-267-986-8
 Sequence 8, Application US/11267986
 Publication No. US2006121554A1
 GENERAL INFORMATION:
 APPLICANT: SHIN, HYUN-CHUL
 APPLICANT: KMON, HEUNG-SUN
 TITLE OF INVENTION: TRANSDUCIBLE DNA-BINDING PROTEINS
 CURRENT APPLICATION NUMBER: US/10/559,806A
 CURRENT FILING DATE: 2005-12-08
 PRIOR APPLICATION NUMBER: PCT/KR04/01385
 PRIOR FILING DATE: 2004-06-10
 PRIOR APPLICATION NUMBER: 60/477,459
 PRIOR FILING DATE: 2003-06-10
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 1
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus
 US-10-559-806A-1

Query Match 55.0%; Score 11; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 APPLICANT: Colamontici, Oscar
 APPLICANT: Sididiqui, Shahnid
 TITLE OF INVENTION: Beta Chain-Associated Regulator of Apoptosis
 FILE REFERENCE: 02-135-D
 CURRENT APPLICATION NUMBER: US/11/267,986
 CURRENT FILING DATE: 2005-11-07
 PRIOR APPLICATION NUMBER: US 60/359,144
 PRIOR FILING DATE: 2002-02-22
 PRIOR APPLICATION NUMBER: US 10/373,288
 PRIOR FILING DATE: 2003-02-24
 PRIOR APPLICATION NUMBER: US 60/625,745
 PRIOR FILING DATE: 2004-11-05
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 8
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE: OTHER INFORMATION: 11 amino acid protein internalization sequence signal based on tL
 OTHER INFORMATION: e HIV tat protein.
 US-11-267-986-8

RESULT 7
 US-11-267-817-19
 Sequence 19, Application US/11267917
 Publication No. US2006148060A1
 GENERAL INFORMATION:
 APPLICANT: LEE, SANG-KYU
 TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic
 ACIDS
 CURRENT APPLICATION NUMBER: US/11/318,535
 CURRENT FILING DATE: 2005-12-28
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 24
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus
 US-11-318-535-24

Query Match 55.0%; Score 11; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 APPLICANT: Karsb, Michael
 TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic
 ACIDS
 CURRENT APPLICATION NUMBER: US/11/318,535
 CURRENT FILING DATE: 2005-12-28
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 24
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus
 US-11-318-535-24

APPLICANT: LEE, SEUNG-KYU
 TITLE OF INVENTION: BIOMOLECULE TRANSDUCTION MOTIF MPH-1-BTM AND THE USE THEREOF
 FILE REFERENCE: 2435.0010002
 CURRENT APPLICATION NUMBER: US/11/267,817
 CURRENT FILING DATE: 2005-11-07
 PRIORITY APPLICATION NUMBER: 10/501,665
 PRIORITY FILING DATE: 2003-01-20
 PRIORITY APPLICATION NUMBER: KR 10-2002-0003183
 PRIORITY FILING DATE: 2002-01-19
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: Kopatent.In 1.71
 SEQ ID NO: 19
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: protein transduction domain
 US-11-267-817-19

Query Match 55.0%; Score 11; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YGRKERRQRR 11
 Db 1 YGRKERRQRR 11

RESULT 8
 US-11-271-285-59
 Sequence 59, Application US/11/271285
 Publication No. US20060148700A1
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Daria
 APPLICANT: Tanaka, Masashi
 APPLICANT: Robbins, Robert C.
 TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted Organ
 FILE REFERENCE: 58600-8218-US00
 CURRENT APPLICATION NUMBER: US/11/271,285
 CURRENT FILING DATE: 2005-11-10
 PRIORITY APPLICATION NUMBER: US 60/626,564
 PRIORITY FILING DATE: 2004-11-10
 NUMBER OF SEQ ID NOS: 59
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 59
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus 1
 US-11-271-285-59

Query Match 55.0%; Score 11; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YGRKERRQRR 11
 Db 1 YGRKERRQRR 11

RESULT 9
 US-11-317-806-85
 Sequence 85, Application US/11/317806
 Publication No. US20060148702A1
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Daria
 APPLICANT: Bright, Daniel
 TITLE OF INVENTION: Methods of Increasing Cerebral Blood Flow
 FILE REFERENCE: 58600-8214-US00
 CURRENT APPLICATION NUMBER: US/11/317,806
 CURRENT FILING DATE: 2005-12-23
 PRIORITY APPLICATION NUMBER: US 60/641,413
 PRIORITY FILING DATE: 2005-01-04

NUMBER OF SEQ ID NOS: 85
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 85
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Human Immunodeficiency Virus 1
 US-11-317-806-85

Query Match 55.0%; Score 11; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKERRQRR 11
 Db 1 YGRKERRQRR 11

RESULT 10
 US-11-238-035-39
 Sequence 39, Application US/11/238035
 Publication No. US2006016081A1
 GENERAL INFORMATION:
 APPLICANT: Luethey, Roland
 APPLICANT: Yang, Robert V.
 APPLICANT: Suggs, Sidney V.
 APPLICANT: Sarosi, Tidiko
 TITLE OF INVENTION: Fibroblast Growth Factor-23 Molecules and Uses Thereof
 FILE REFERENCE: 01-004
 CURRENT APPLICATION NUMBER: US/11/238,035
 CURRENT FILING DATE: 2005-09-28
 NUMBER OF SEQ ID NOS: 54
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 39
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus type 1
 US-11-238-035-39

Query Match 55.0%; Score 11; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKERRQRR 11
 Db 1 YGRKERRQRR 11

RESULT 11
 US-11-250-830-1
 Sequence 1, Application US/11/250830
 Publication No. US20060159019A1
 GENERAL INFORMATION:
 APPLICANT: BECKER, MATTHEW L.
 APPLICANT: FANG, HUAFENG
 APPLICANT: LI, XIAOQU
 APPLICANT: PAN, DIPANJAN
 APPLICANT: ROSSIN, RAFFAELLA
 APPLICANT: SUN, XIANKAI
 APPLICANT: TAYLOR, JOHN STEPHEN
 APPLICANT: TURNER, JEFFREY L.
 APPLICANT: WELCH, MICHAEL JOHN
 APPLICANT: WOOLLEY, KAREN L.
 TITLE OF INVENTION: CELL PERMEABLE NANOCONJUGATES OF SHELL-CROSSLINKED KNEDEL (SCK) AND PEPTIDE NUCLEIC ACIDS ("PNAs") WITH UNIQUELY EXPRESSED OR OVER-EXPRESSED mRNA TARGETING SEQUENCES FOR EARLY DIAGNOSIS AND THERAPY OF CANCER
 CURRENT APPLICATION NUMBER: US/11/250,830
 CURRENT FILING DATE: 2005-10-14
 PRIORITY APPLICATION NUMBER: 60/619,242
 PRIORITY FILING DATE: 2004-10-15
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: PatentIn Ver. 3.3

SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-250-830-1

Query Match Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKRRQRQQ 11
Db 1 YGRKRRQRQQ 11

RESULT 14
US-11-142-051-4
; Sequence 4, Application US/11142051
; Publication No. US20061010956A1
; GENERAL INFORMATION:
; APPLICANT: Pincus, Matthew
; APPLICANT: Michl, Josef
; TITLE OF INVENTION: PHENOTYPIC REVERSION OF PANCREATIC CARCINOMA CELLS
; FILE REFERENCE: 1181-26
; CURRENT APPLICATION NUMBER: US/11/142,051
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: US 60/575,131
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/575,846
; PRIOR FILING DATE: 2004-05-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
; TYPE: PRT
; LENGTH: 14
; ORGANISM: Artificial
; FEATURE: peptide; HIV-1 TAT membrane penetrating sequence
US-11-142-051-4

Query Match 55.0%; Score 11; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKRRQRQQ 11
Db 1 YGRKRRQRQQ 11

RESULT 15
US-11-318-535-7
; Sequence 7, Application US/11318535
; Publication No. US2006106197A1
; GENERAL INFORMATION:
; APPLICANT: Karab, Michael
; TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic
; ACIDS
; FILE REFERENCE: 002877_00028
; CURRENT APPLICATION NUMBER: US/11/318,535
; CURRENT FILING DATE: 2005-12-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: protein transduction domain
; NAME/KEY: MIS-C FEATURE
; LOCATION: (1).-(1)
; OTHER INFORMATION: Biotin

Qy 1 YGRKRRQRQQ 11
Db 1 YGRKRRQRQQ 11

RESULT 13
US-11-264-074-19
; Sequence 19, Application US/11264074
; Publication No. US20061048104A1
; GENERAL INFORMATION:
; APPLICANT: Marin, et al
; TITLE OF INVENTION: Detection and Ion Channel or Receptor Activity
; FILE REFERENCE: 0492611-0647
; CURRENT APPLICATION NUMBER: US/11/264,074
; CURRENT FILING DATE: 2005-10-31
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: TAT peptide

Qy 1 YGRKRRQRQQ 11
Db 4 YGRKRRQRQQ 14

Query Match 55.0%; Score 11; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0001; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKRRQRQQ 11
Db 4 YGRKRRQRQQ 14

Search completed: August 24, 2006, 23:56:54
Job time : 32 secs

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OM protein - protein search, using SW model

Run on: August 24, 2006 23:46:43 ; Search time 38 Seconds (without alignments)

50.640 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 20

Sequence: 1 YGRKRRQRRKPADGHR 20

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs., 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 80:*

- 1: pir1:*
- 2: pir2:*
- 3: pir3:*
- 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	11	55.0	71	2	T09384		trans-activating t
2	11	55.0	72	1	TNLJH4		trans-activating t
3	11	55.0	86	1	TNLJZR		trans-activating t
4	11	55.0	86	2	A25700		trans-activating t
5	11	55.0	86	2	JCS591		trans-activator pro
6	11	55.0	86	2	S53181		tat protein - huma
7	11	55.0	86	2	S33382		trans-activating t
8	11	55.0	87	2	T01665		tat protein - huma
9	11	55.0	95	1	TNLJ12		trans-activating t
10	11	55.0	101	1	E4001		trans-activating t
11	11	55.0	101	2	T09446		tat protein - huma
12	10	50.0	86	1	TNLJND		trans-activating t
13	9	45.0	541	1	A43610		protein-tyrosine K
14	9	45.0	542	1	TVIUSC		probable pilin Ngr
15	7	35.0	143	2	AE2781		hypothetical prote
16	7	35.0	668	2	T29884		hypothetical prote
17	7	35.0	1951	2	S00320		sodium channel pro
18	7	35.0	1983	2	A60054		ribosomal protein
19	6	30.0	29	2	S08555		probable 50S ribos
20	6	30.0	46	2	A10560		probable pilin Ngr
21	6	30.0	53	4	S10048		hypothetical prote
22	6	30.0	78	2	E97064		NO! protein, nitra
23	6	30.0	80	2	T01320		hypothetical prote
24	6	30.0	81	2	C95394		transport protein
25	6	30.0	81	2	T47865		trans-activating t
26	6	30.0	100	1	TNLJSI		trans-regulatory s
27	6	30.0	103	1	VKLJGG		trans-regulatory s
28	6	30.0	108	2	VKLJS2		vira/G regulated p
29	6	30.0	108	2	A13250		

ALIGNMENTS

RESULT 1
T09384
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate HIV-1)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 31-Dec-2004
C;Accession: T09384
R;Michael, N.L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.; Bir
J. Virol. 69, 4228-4236, 1995
A;Title: Defective accessory genes in a human immunodeficiency virus type 1-infected lor
A;Reference number: Z16654; PMID: 95287475; PMID: 7769682
A;Accession: T09384
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-71 <MIC>
A;Cross-references: UNIPARC:Q71926; UNIPARC:UPI00000FF00C; EMBL:U24451; NID:g829440; PI
C;Genetics:
A;Gene: tat
C;Superfamily: leukemia virus trans-activating transcription regulator
C;Keywords: transcription

Query Match 55.0%; Score 11; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKERRQRR 11
Db 47 YGRKERRQRR 57

RESULT 2
TNLJH4
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate HIV-1)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004
C;Accession: B25523
R;Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare,
Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986
A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human
A;Reference number: A94136; PMID: 87041461; PMID: 3490666
A;Accession: B25523
A;Molecule type: DNA
A;Residues: 1-72 <DE5>
A;Cross-references: UNIPARC:UPI000174A5; GB:MI1337; NID:g126460
A;Note: the GenBank entry ADRE3AA differs from the published sequence in tra
C;Genetics:
A;Gene: tat
C;Superfamily: transcription regulation
C;Keywords: transcription regulation

Query Match 55.0%; Score 11; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 3
 TNLJZR
 Trans-activating transcription regulator - human immunodeficiency virus Zr-6
 C;Species: human immunodeficiency virus Zr-6
 C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 31-Dec-2004
 A;Accession: C26192
 R;Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Fehrino, P.; Schochetman, G.; Cu
 Gene 52, 71-82, 1987
 A;Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleot
 A;Reference number: A26192; MUID:87248097; PMID:3036660
 A;Accession: C26192
 A;Molecule type: DNA
 A;Residues: 1-86 <SRI>
 A;Cross-references: UNIPROT:P04609; UNIPARC:UPI000013693A; GB:K03458; GB:M16322; NID:932
 A;Gene: tat
 A;Introns: 72/3
 C;Superfamily: leukemia virus trans-activating transcription regulator
 C;Keywords: AIDS; immunodeficiency; transcription regulation
 Query Match 4
 A25700
 Trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 31-Dec-2004
 C;Accession: A25700
 R;Sodroski, J.; Patarca, R.; Rosen, C.; Wong-Staal, F.; Haseltine, W.
 Science 229, 74-77, 1985
 A;Reference number: A25700; MUID:85244627; PMID:2990041
 A;Accession: A25700
 A;Status: Preliminary
 A;Molecule type: mRNA
 A;Residues: 1-86 <SOD>
 A;Cross-references: UNIPROT:P04610; UNIPARC:UPI0000111F40
 C;Superfamily: leukemia virus trans-activating transcription regulator
 Query Match 5
 JC5591
 Transactivator protein - human immunodeficiency virus type 1
 N;Alternate names: tat protein
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Accession: JC5591
 R;Hoffmann, S.; Willbold, D.
 Biochem. Biophys. Res. Commun. 235, 806-811, 1997
 A;Title: A selection system to study protein-RNA interactions: Functional display of HIV
 A;Reference number: JC5591; MUID:97350867; PMID:9207243
 A;Accession: JC5591
 A;Molecule type: protein

A;Residues: 1-86 <H02>
 A;Cross-references: UNIPARC:UPI000017865E
 C;Comment: This protein is a key regulatory protein in the viral replication cycle and b
 C;Superfamily: leukemia virus trans-activating transcription regulator
 F;22-31/Region: cysteine-rich

Query Match 6
 YGRKKRRQRRR 11
 Best Local Similarity 100.0%; Pred. No. 0.00039; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRR 11
 Db 47 YGRKKRRQRRR 57

RESULT 6
 S54381
 tat protein - human immunodeficiency virus type 1
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 31-Dec-2004
 C;Accession: S54381
 R;Theodore, T.; Buckler-White, A.J.
 submitted to the EMBL Data Library, July 1989
 A;Reference number: S54381
 A;Accession: S54381
 A;Status: preliminary
 A;Molecule type: Genomic RNA
 A;Residues: 1-86 <THB>
 A;Cross-references: UNIPROT:P12506; UNIPARC:UPI000013693B; EMBL:M22639; NID:9329377; PID:
 C;Genetics:
 A;Introns: 72/2
 C;Superfamily: leukemia virus trans-activating transcription regulator
 Query Match 7
 YGRKKRRQRRR 11
 Best Local Similarity 100.0%; Pred. No. 0.00039; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRR 11
 Db 47 YGRKKRRQRRR 57

RESULT 7
 S33982
 trans-activating transcription regulator - human immunodeficiency virus type 1
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 06-Oct-1994 #sequence_revision 23-Feb-1996 #text_change 31-Dec-2004
 C;Accession: S33982; S226305; S19864
 R;Carlini, F.
 submitted to the EMBL Data Library, November 1991
 A;Reference number: S33979
 A;Accession: S33982
 A;Molecule type: DNA
 A;Residues: 1-86 <CAR>
 A;Cross references: UNIPROT:P04606; UNIPARC:UPI0000000419; EMBL:Z11530; NID:960192; PID:
 R;Siderovskii, D.P.; Matsuyama, T.; Prigerio, E.; Chui, S.; Min, X.; Erie, H.; Sumner-Su
 Nucleic Acids Res. 20, 5311-5320, 1992
 A;Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activator c
 A;Reference number: S26385; MUID:9305196; PMID:1437550
 A;Accession: S26385
 A;Molecule type: nucleic acid
 A;Residues: 1-86 <SID>
 A;Cross references: UNIPARC:UPI0000000419; EMBL:X64650; NID:960144; PID:CAA45921.1; PI
 C;Genetics:
 A;Gene: tat
 A;Introns: 72/2
 C;Superfamily: leukemia virus trans-activating transcription regulator
 Query Match 8
 Best Local Similarity 100.0%; Pred. No. 0.00039; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRR 11
 Db 47 YGRKKRRQRRR 57

RESULT 5
 JC5591
 transactivator protein - human immunodeficiency virus type 1
 N;Alternate names: tat protein
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Accession: JC5591
 R;Hoffmann, S.; Willbold, D.
 Biochem. Biophys. Res. Commun. 235, 806-811, 1997
 A;Title: A selection system to study protein-RNA interactions: Functional display of HIV
 A;Reference number: JC5591; MUID:97350867; PMID:9207243
 A;Accession: JC5591
 A;Molecule type: protein

Qy 1 YGRKKRQRRR 11
Db 47 YGRKKRQRRR 57

RESULT 8
T01665
tat protein - human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Accession: T01665
R;Allison, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isolates
A;Reference number: Z14389; MUID:86245056; PMID:2424612
A;Accession: T01665
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-87 <Ali>
A;Cross-references: UNIPROT:P04613; UNIPARC:UPI00001132A9; EMBL:K03456; NID:g60228; PIDN
C;Genetics:
A;Introns: 72/2
C;Superfamily: leukemia virus trans-activating transcription regulator

Query Match 55.0%; Score 11; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 11; Conservative 0; Gaps 0;
Indels 0; Mismatches 0;

Qy 1 YGRKKRQRRR 11
Db 47 YGRKKRQRRR 57

RESULT 9
TNLJ12
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate A;Note: host Homo sapiens (man))
C;Accession: A04017
R;Arya, S.K.; Gallo, R.C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986
A;Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity of A;Reference number: A94093; MUID:86177573; PMID:3008154
A;Accession: A04017
A;Molecule type: DNA
A;Residues: 1-95 <ARV>
A;Cross-references: UNIPROT:P04326; UNIPARC:UPI0000174A54
C;Genetics:
A;Gene: tat
C;Superfamily: leukemia virus trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 55.0%; Score 11; DB 1; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 11; Conservative 0; Gaps 0;
Indels 0; Mismatches 0;

Qy 1 YGRKKRQRRR 11
Db 56 YGRKKRQRRR 66

RESULT 10
E44001
trans-activating transcription regulator - human immunodeficiency virus type 1 (strain Y)
N;Alternate names: tat protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man))
C;Accession: E44001
R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6577-6580, 1992
A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; MUID:93021387; PMID:1404605
A;Accession: E44001
A;Molecule type: DNA
A;Residues: 1-101 <LY>
A;Cross-references: UNIPROT:P35965; UNIPARC:UPI0000136937; GB:M93258
C;Genetics:
A;Gene: tat
A;Introns: 72/2
C;Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 55.0%; Score 11; DB 1; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 11; Conservative 0; Gaps 0;
Indels 0; Mismatches 0;

Qy 1 YGRKKRQRRR 11
Db 47 YGRKKRQRRR 57

RESULT 11
T09446
tat protein - human immunodeficiency virus type 1 (strain JRFL)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004
C;Accession: T09446
R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submitted to the EMBL Data Library, July 1996
A;Reference number: Z16673
A;Accession: T09446
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-101 <PAN>
A;Cross-references: UNIPROT:Q75758; UNIPARC:UPI0000109776; EMBL:U63632; NID:g1465777; EMBL:U63632; NID:g1465777; PI

C;Genetics:
A;Gene: tat
A;Introns: 72/2
C;Superfamily: leukemia virus trans-activating transcription regulator

Query Match 55.0%; Score 11; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 11; Conservative 0; Gaps 0;
Indels 0; Mismatches 0;

Qy 1 YGRKKRQRRR 11
Db 47 YGRKKRQRRR 57

RESULT 12
TNLJND
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate A;Note: host Homo sapiens (man))
C;Accession: J00071
R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A., Gene 81, 275-284, 1989
A;Title: Nucleotide sequence of HIV1-NFK: a highly cytopathic strain of the human immunodeficiency virus
A;Reference number: JQ0071
A;Accession: JQ0071
A;Molecule type: DNA
A;Residues: 1-86 <SP1>
A;Cross-references: UNIPROT:P18804; UNIPARC:UPI000011D5D6; GB:M27323; NID:9328154; PIDN:
C;Genetics:
A;Gene: tat
C;Superfamily: leukemia virus trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency; transcription

Query Match 50.0%; Score 10; DB 1; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 10; Conservative 0; Gaps 0;
Indels 0; Mismatches 0;

Qy 1 YGRKKRQRRR 10

Db 47 YRKRRQR 56

RESULT 13

A43610 Protein-tyrosine kinase (EC 2.7.1.112) src, neuronal [similarity] - mouse
 N; Alternate names: Rous sarcoma oncogene
 C; Species: Mus musculus (house mouse)
 C; Accession: A43610
 C; Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
 R; Martinez, R.; Mathey-Prevot, B.; Bernards, A.; Baltimore, D.
 Science 237, 411-415, 1987
 Article: Neuronal pp6(c-src) contains a six-amino acid insertion relative to its non-neuronal pp6(c-src) - PMID:87263406; PMID:2440106
 A; Reference number: A43610
 A; Accession: A43610
 A; Molecule type: mRNA
 A; Residues: 1-541 <PAPR>
 A; Cross-references: UNIPARC:UP05480; UNIPARC:UPI0000161D19; GB:MI17031; NID:G201056; PIDN:
 C; Comment: The neuronal c-src has an 6 residue insertion of RLVNR within the amino-terminal
 C; Genetics:
 A; Gene: Src
 A; Cross-references: MGI: 98397
 A; Map position: 2:91.0
 A; Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
 C; Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phosphatase
 P:90-145/Domain: SH3 homology <SH3>
 P:156-253/Domain: SH2 homology <SH2>
 P:273-531/Domain: protein kinase homology <KIN>
 P:281-389/Region: protein kinase ATP-binding motif
 P:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 P:3/03/Active site: Lys #status predicted
 P:424,535/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 P:425,536/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 Query Match 45.0%; Score 9; DB 1; Length 541;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 KPASADGHR 20
 Db 39 KPASADGHR 47

RESULT 14

TWRSUC Protein-tyrosine kinase (EC 2.7.1.112) src, neuronal - human
 C; Species: Homo sapiens (man)
 C; Date: 30-Jun-1989 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
 C; Accession: A26891; A61083; B61083; A23287; A28832; B34704
 R; Tanaka, A.; Gibbs, C.P.; Arthur, R.R.; Anderson, S.K.; Kung, H.J.; Fujita, D.J.
 Mol. Cell. Biol. 7, 1978-1983, 1987
 Article: DNA sequence encoding the amino-terminal region of the human c-src protein: img
 A; Reference number: A26891; MUID:87257903; PMID:3293057
 A; Accession: A26891
 A; Molecule type: mRNA
 A; Residues: 1-117-124-191 <TAN>
 A; Cross-references: UNIPARC:PI12931; UNIPARC:UPI0000172579; GB:M16
 R; Pyper, J.M.; Bolen, J.B.
 J. Neurosci. Res. 24, 89-96, 1989
 Article: Neuron-specific splicing of C-SRC RNA in human brain.
 A; Reference number: A61083; MUID:90040822; PMID:2681803
 A; Accession: A61083
 A; Molecule type: mRNA
 A; Residues: 98-145 <PYP>
 A; Cross-references: UNIPARC:UPI000017257A
 A; Accession: B61083
 A; Molecule type: mRNA
 A; Residues: 98-117-124-145 <PY2>
 A; Cross-references: UNIPARC:UPI000017257A
 R; Anderson, S.K.; Gibbs, C.P.; Tanaka, A.; Kung, H.J.; Fujita, D.J.
 Mol. Cell. Biol. 5, 1122-1129, 1985
 Article: Human cellular src gene: Nucleotide sequence and derived amino acid sequence of
 A; Reference number: A23287; MUID:85213483; PMID:2582238

RESULT 15

hypothetical protein Atu1668 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)|
 C; Species: Agrobacterium tumefaciens
 C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C; Accession: AF2781
 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, T.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, J.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
 A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, R.; W.; Steer, E.
 A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A; Reference number: AB2577; MUID:21608550; PMID:11743193
 A; Accession: AF2781
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-143 <KUR>
 A; Cross references: UNIPROT:Q8UBT7; UNIPARC:UPI00000D1C2E; GB:AE008688; PIDN:AAL42668.1
 C; Generics:
 A; Gene: Atu1668
 A; Map position: circular chromosome

Query Match 35.0%; Score 7; DB 2; Length 143;

Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy	5 KRRRKK	11
Db	41 KRRQRR	47

Search completed: August 24, 2006, 23:52:12
Job time : 40 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd.	GenCore version 5.1.9										
protein - protein search, using SW mode!											
on: August 24, 2006, 23:43:13 ; Search time 300 Seconds (without alignments)											
61.668 Million cell updates/sec											
le: US-10-814-109-2											
effect score: 20											
quence: 1 YGRKQKRQRKKPASADGHR 20											
oring table: OLIGO											
Gapop 60.0 , Gapext 60.0											
atched:	2849598 seqs, 925015592 residues										
nd size :	1										
al number of hits satisfying chosen parameters:	28495979										
imum DB seq length: 0											
imum DB seq length: 2000000000											
t-processing: Listing first 45 summaries											
atabase : UniProt 7.2.*	1: uniprot_sprot: 2: uniprot_trembl: *										
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.											
SUMMARIES											
ult	Score	Query	Match	Length	DB	ID	Description				
No.											
1	12	60.0	86	2	Q6Y0V6_9HIV1		Q6Y0V6 human immun				
2	11	55.0	58	1	TAT_HIV1		P04612 human immun				
3	11	55.0	64	2	Q6QAV2_9HIV1		Q6QAV2 human immun				
4	11	55.0	65	2	Q75542_9HIV1		Q75540 human immun				
5	11	55.0	65	2	Q75544_9HIV1		Q75544 human immun				
6	11	55.0	68	2	Q6QAV4_9HIV1		Q6QAV4 human immun				
7	11	55.0	70	2	Q6EMQ1_9HIV1		Q6EMQ1 human immun				
8	11	55.0	71	2	Q40224_9HIV1		Q40224 human immun				
9	11	55.0	71	2	Q40225_9HIV1		Q40225 human immun				
10	11	55.0	71	2	Q40226_9HIV1		Q40226 human immun				
11	11	55.0	71	2	Q40227_9HIV1		Q40227 human immun				
12	11	55.0	71	2	Q40228_9HIV1		Q40228 human immun				
13	11	55.0	71	2	Q40231_9HIV1		Q40231 human immun				
14	11	55.0	71	2	Q40232_9HIV1		Q40232 human immun				
15	11	55.0	71	2	Q40233_9HIV1		Q40233 human immun				
16	11	55.0	71	2	Q40234_9HIV1		Q40234 human immun				
17	11	55.0	71	2	Q3S9T9_9HIV1		Q3S9T9 human immun				
18	11	55.0	71	2	Q3S9U5_9HIV1		Q3S9U5 human immun				
19	11	55.0	71	2	Q3S9W0_9HIV1		Q3S9W0 human immun				
20	11	55.0	71	2	Q3S9NB_9HIV1		Q3S9NB human immun				
21	11	55.0	71	2	Q5BP71_9HIV1		Q5BP71 human immun				
22	11	55.0	71	2	Q5BQ03_9HIV1		Q5BQ03 human immun				
23	11	55.0	71	2	Q5BQ10_9HIV1		Q5BQ10 human immun				
24	11	55.0	71	2	Q5Q64_9HIV1		Q5Q64 human immun				
25	11	55.0	71	2	Q5BQ69_9HIV1		Q5BQ69 human immun				
26	11	55.0	71	2	Q5G7B5_9HIV1		Q5G7B5 human immun				
27	11	55.0	71	2	Q5UG44_9HIV1		Q5UG44 human immun				
28	11	55.0	71	2	Q5UG61_9HIV1		Q5UG61 human immun				
29	11	55.0	71	2	Q5UG65_9HIV1		Q5UG65 human immun				
30	11	55.0	71	2	Q5UG66_9HIV1		Q5UG66 human immun				
31	11	55.0	71	2	Q5UG67_9HIV1		Q5UG67 human immun				
32	11	55.0	71	2	Q5UG48_9HIV1		Q5UG48 human immun				
33	11	55.0	71	2	Q5UG52_9HIV1		Q5UG52 human immun				
34	11	55.0	71	2	Q5UG53_9HIV1		Q5UG53 human immun				
35	11	55.0	71	2	Q5UG54_9HIV1		Q5UG54 human immun				
36	11	55.0	71	2	Q5UG55_9HIV1		Q5UG55 human immun				
37	11	55.0	71	2	Q5UG56_9HIV1		Q5UG56 human immun				
38	11	55.0	71	2	Q5UG57_9HIV1		Q5UG57 human immun				
39	11	55.0	71	2	Q5UG58_9HIV1		Q5UG58 human immun				
40	11	55.0	71	2	Q5UG59_9HIV1		Q5UG59 human immun				
41	11	55.0	71	2	Q5UG60_9HIV1		Q5UG60 human immun				
42	11	55.0	71	2	Q5UG61_9HIV1		Q5UG61 human immun				
43	11	55.0	71	2	Q5UG62_9HIV1		Q5UG62 human immun				
44	11	55.0	71	2	Q5UG64_9HIV1		Q5UG64 human immun				
45	11	55.0	71	2	Q5UG65_9HIV1		Q5UG65 human immun				

RESULT 2				
TAT_HVIB5	STANDARD;	PRT;	58 AA.	
ID HVIB5				
AC P04612;				
DT 13-AUG-1987; integrated into UniProtKB/Swiss-Prot.				
DT 13-AUG-1987; sequence version 1.				
DT 07-FEB-2006; entry version 40.				
DB TAT protein (Transactivating regulatory protein) (Fragment).				
GS Human immunodeficiency virus type 1 (isolate BH5) (HIV-1).				
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;				
CC Lentiviruses; Primate lentivirus group.				
OX NCBI_TaxID:11682;				
RN RNP_SEQUENCE [GENOMIC RNA].				
REVIEWED; MEDLINE:85111123; PubMed:278615;				
RA Ratner L., Haseltine W.A., Patarca R., Livak K.J., Starcich B.R.,				
RA Baumeister K., Doran E.R., Rafalski J.A., Whitehorn B.A.,				
RA Baumeister K., Ivanoff L., Petterway S.R. Jr., Pearson M.L.,				
RA Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C.,				
RA Wong-Staal F.,				
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";				
RL Nature 313:277-284(1985).				
CC -1 FUNCTION: Transcriptional regulator that acts by binding to the trans-activating responsive sequence (TAR) RNA element and activates transcription initiation and/or elongation from the LTR promoter.				
CC -1 SUBUNIT: Binds cyclin T1 (By similarity).				
CC -1 SUBCELLULAR LOCATION: Nuclear; nucleolar.				
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms				
CC Distributed under the Creative Commons Attribution-NoDerivs License				
CC				
DR EMBL; K02012; AAA14656.1; -; Genomic_RNA.				
DR HSSP; P04610; 1JFW.				
DR SMR; P04612; 1A7.				
DR HIV; K02012; TATBH5.				
DR InterPro; IPR001831; IV_Tat.				
DR Pfam; PF00539; Tat_1.				
DR PRINTS; PRO0055; HIVTDOMAIN.				
DR Activator; AIDS; Nuclear protein; RNA-binding; Transcription; CHAIN 1 >58 TAT protein.				
FT NON_TER /FTId=PRO_0000085343.				
FT NON_TER 58 AA; 58 MW; E36C21F8FD812E3 CRC64;				
FT SEQUENCE 58 AA; 6800 MW; E36C21F8FD812E3 CRC64;				
Query Match 55.0%; Score 11; DB 1; Length 58;				
Best Local Similarity 100.0%; Pred. No. 0.00083;				
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY 1 YGRKRRQRQR 11				
DB 47 YGRKRRQRQR 57				
RESULT 3				
Q6QAV2_9HIV1	PRELIMINARY;	PRT;	64 AA.	
ID Q6QAV2_9HIV1				
AC Q6QAV2_				
DT 05-JUL-2004; integrated into UniProtKB/TrEMBL.				
DT 05-JUL-2004; sequence version 1.				
DT 05-FEB-2006; entry version 10.				
DB Tat protein (Fragment).				
GS Human immunodeficiency virus 1.				
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;				
CC Lentiviruses; Primate lentivirus group.				
OX NCBI_TaxID:11676;				
RN [1]				
RP NUCLEOTIDE SEQUENCE [9HIV1 PRELIMINARY; PRT; 64 AA.				
RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.; DR GO:0003723; F:RNA binding; IEA.				
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.				
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms				
CC Distributed under the Creative Commons Attribution-NoDerivs License				
DR GO: U57244; AA17808.1; -; Genomic_DNA.				
DR HSPP; P125056; 1TBC.				
DR GO: GO:0005634; C:host cell nucleus; IEA.				
DR GO: GO:0003723; F:RNA binding; IEA.				
DR GO: GO:0042025; P:transcription factor activity; IEA.				
DR GO: GO:0006355; P:transcription of transcr. factor activity; IEA.				
DR GO: GO:0006350; P:transcription; IEA.				
DR InterPro; IPR001831; IV_Tat.				
DR Pfam; PF00539; Tat_1.				
DR PRINTS; PRO0055; HIVTDOMAIN.				
DR Activator; Nuclear protein; RNA-binding; Transcription; CHAIN 1 >1 YGRKRRQRQR 57				
FT NON_TER 65 AA; 7619 MW; 91584F861A2F9736 CRC64;				
FT SEQUENCE 65 AA; 7619 MW; 91584F861A2F9736 CRC64;				
Query Match 55.0%; Score 11; DB 2; Length 65;				
Best Local Similarity 100.0%; Pred. No. 0.00092;				
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

NUCLEOTIDE SEQUENCE [9HIV1 PRELIMINARY; PRT; 64 AA.]
PubMed=15157352; DOI=10.1089/0889220423048087;
Andreo S.M.S., Barra L.A.C., Costa L.J., Sucupira M.C.A.,

Qy	1 YGRKKRQRRR 11	CC	Distributed under the Creative Commons Attribution-NoDerivs License
Db	47 YGRKKRQRRR 57	CC	
RESULT 5		DR	SMR; Q6QAV4_1-68;
Q75544_9HIV1	PRELIMINARY; PRT; 65 AA.	DR	GO; GO:0042025; C:host cell nucleus; IEA.
ID Q75544_9HIV1	Integrated into UniProtKB/T-EMBL.	DR	GO; GO:0005634; C:nucleus; IEA.
AC Q75544_9HIV1	01-NOV-1996, sequence version 1.	DR	GO; GO:003723; F:RNA binding; IEA.
DT 01-NOV-1996	07-FEB-2006, entry version 26.	DR	GO; GO:0003700; F:transcription factor activity; IEA.
DR	Tat protein (Fragment).	DR	GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
GN Name=tat;		DR	InterPro; IPR01831; IV_Tat.
OS Human immunodeficiency virus 1.		DR	Pfam; PF00539; Tat; 1.
OC Lentivirus; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;		DR	PRINTS; PR00055; HIVTATDOMAIN.
OX NCBI_TaxID=11676;		KW	Activator; Nuclear protein; RNA-binding; Transcription; KW Transcription regulation.
RN [1]		FT	NON TER 1 1
RP NUCLEOTIDE SEQUENCE.		SQ	SEQUENCE 68 AA; 7983 MW; 326A05D50078CD29 CRC64;
RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;		Query Match	55.0%; Score 11; DB 2; Length 68;
RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.		Best Local Similarity	100.0%; Pred. No. 0.00095;
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms		Matches	0; Mismatches 0; Indels 0; Gaps 0;
CC Distributed under the Creative Commons Attribution-NoDerivs License		Qy	1 YGRKKRQRRR 11
CC		Db	43 YGRKKRQRRR 53
DR U57252; ARB17812.1; - ; Genomic_DNA.		RESULT 7	
DR HSSP; IP2506; ITPC.		Q66MQ1_9HIV1	
DR GO; GO:0042025; C:host cell nucleus; IEA.		ID Q66MQ1_9HIV1	PRELIMINARY; PRT; 70 AA.
DR GO; GO:0005634; C:nucleus; IEA.		AC Q66MQ1_9HIV1	
DR GO; GO:0003723; F:RNA binding; IEA.		DT 11-OCT-2004, integrated into UniProtKB/TREMBL.	
DR GO; GO:0003700; F:transcription factor activity; IEA.		DT 11-OCT-2004, sequence version 1.	
DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.		DT 07-FEB-2006, entry version 8.	
DR InterPro; IPR001831; IV_Tat.		DB Tat protein (Fragment).	
DR Pfam; PF00539; Tat; 1.		GN Name=tat;	
DR PRINTS; PR00055; HIVTATDOMAIN.		OS Human immunodeficiency virus 1.	
KW Activator; Nuclear protein; RNA-binding; Transcription; KW Transcription regulation.		OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; OC Lentivirus; Primate lentivirus group.	
FT NON TER 1 1		RN [1]	NCBI_TaxID=11676;
SQ SEQUENCE 65 AA; 7677 MW; 91584F861F6A8362 CRC64;		RP NUCLEOTIDE SEQUENCE.	
Query Match	55.0%; Score 11; DB 2; Length 65;	RA Herring B.L., Grant R.M., Delwart E.L.;	
Best Local Similarity	100.0%; Pred. No. 0.00092;	RA RT "No superinfection among seroconcordant couples after well-defined	
Matches	0; Mismatches 0; Indels 0; Gaps 0;	RT exposure.";	
Qy	1 YGRKKRQRRR 11	RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.	
Db	47 YGRKKRQRRR 57	CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
RESULT 6		CC	Distributed under the Creative Commons Attribution-NoDerivs License
Q6QAV4_9HIV1	PRELIMINARY; PRT; 68 AA.	DR	EMBL; AY686119; AU005440.1; - ; Genomic_RNA.
ID Q6QAV4_9HIV1	Integrated into UniProtKB/T-EMBL.	DR	SMR; Q66MQ1_1-70.
AC Q6QAV4_9HIV1	05-JUL-2004, sequence version 1.	DR	GO; GO:0042025; C:host cell nucleus; IEA.
DT 05-JUL-2004	05-JUL-2004, sequence version 10.	DR	GO; GO:0005634; C:nucleus; IEA.
DR	Tat protein (Fragment).	DR	GO; GO:003723; F:RNA binding; IEA.
GN Name=tat;		DR	GO; GO:0003700; F:transcription factor activity; IEA.
OS Human immunodeficiency virus 1.		DR	GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
OC Lentivirus; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;		DR	InterPro; IPR01831; IV_Tat.
OC Lentivirus; Primate lentivirus group.		DR	Pfam; PF00539; Tat; 1.
OX NCBI_TaxID=11676;		DR	PRINTS; PR00055; HIVTATDOMAIN.
RN [1]		KW Activator; Nuclear protein; RNA-binding; Transcription; KW Transcription regulation.	
RP NUCLEOTIDE SEQUENCE.		FT	NON TER 70 70
RX PubMed:1517352; DOI=10.1089/08892204323048087;		SQ	SEQUENCE 8096 MW; 28E39B5672863DBB CRC64;
RA Andreo S.M.S., Barra L.A.C., Costa L.J., Sucupira M.C.A., Souza I.B.L., Diaz R.S.;		Query Match	55.0%; Score 11; DB 2; Length 70;
RA "HIV Type 1 Transmission by Human Bite.";		Best Local Similarity	100.0%; Pred. No. 0.00098;
RL AIDS Res. Hum. Retroviruses 20:349-350 (2004).		Matches	0; Mismatches 0; Indels 0; Gaps 0;
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CC		Db	47 YGRKKRQRRR 57

RESULT 8		RA Desrosiers R.C.; "Activity of human immunodeficiency virus type 1 promoter/TAR regions and tat1 genes derived from individuals with different rates of disease progression."; RT
040224_9HIV1	PRELIMINARY;	RT
ID	PRT;	RT
AC 040224;	71 AA.	RT
AC 040224_9HIV1		RT
DT 01-JAN-1998,	integrated into UniProtKB/TrEMBL.	RT
DT 01-JAN-1998,	see http://www.uniprot.org/terms	RT
DT 07-FEB-2006,	entry version 25.	RT
DE Tat protein (Fragment).		RT
GN Name=tat;		RT
OS Human immunodeficiency virus 1.		RT
OC Virus; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;		RT
OC Lentivirus; Primate lentivirus group.		RT
OX NCBI_TAXID=1676;		RT
RN [1]		RT
RP NUCLEOTIDE SEQUENCE.		RT
RX STRAIN=AD93_A3cat;		RT
MEDLINE=9735179; PubMed=9191845; DOI=10.1006/viro.1997.8586;		RT
RA Kirchhoff, P., Greenough T.C., Hamacher M., Sullivan J.L., Desrosiers R.C.;		RT
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions and tat1 genes derived from individuals with different rates of disease progression."		RT
RT Virology 233:319-331 (1997).		RT
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DR EMBL; AF00522; AAB62521.1; -; Genomic_DNA.		RT
DR HSSP; P04610; 1JFW.		RT
DR SMR; O00224; 1-71.		RT
DR GO; GO:0042025; C:host cell nucleus; IEA.		RT
DR GO; GO:0005634; C:nucleus; IEA.		RT
DR GO; GO:0003723; F:RNA binding; IEA.		RT
DR GO; GO:0003700; F:transcription factor activity; IEA.		RT
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.		RT
DR InterPro; IPR001831; IV_Tat.		RT
DR Pfam; PF00539; Tat; 1.		RT
DR PRINTS; PR00055; HIVATDOMAIN.		RT
KW Activator; Nuclear protein; RNA-binding; Transcription;		RT
KW Transcription regulation.		RT
FT NON_TER		RT
SEQUENCE 71 AA; 8179 MW; CE411588EB96200F CRC64;		RT
Query Match 55.0%; Score 11; DB 2; Length 71;		RT
Best Local Similarity 100.0%; Pred. No. 0.00099;		RT
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		RT
QY 1 YGRKERRQRRR 11		RT
DB 47 YGRKERRQRRR 57		RT
RESULT 10		RT
040226_9HIV1	PRELIMINARY;	RT
ID Q40226_9HIV1		RT
DR Q40226;		RT
AC 040226;		RT
DR DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.		RT
DR DT 01-JAN-1998, sequence version 1.		RT
DR DT 07-FEB-2006, entry version 25.		RT
DE Tat protein (Fragment).		RT
GN Name=tat;		RT
OS Human immunodeficiency virus 1.		RT
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;		RT
OC Lentivirus; Primate lentivirus group.		RT
RN [1]		RT
RP NUCLEOTIDE SEQUENCE.		RT
SQ STRAIN=B794_A2rat;		RT
DR RX PMID=9735179; PubMed=9191845; DOI=10.1006/viro.1997.8586;		RT
RA RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L., Desrosiers R.C.;		RT
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions and tat1 genes derived from individuals with different rates of disease progression."		RT
RT Virology 233:319-331 (1997).		RT
DR HSSP; P04610; 1JFW.		RT
DR SMR; O40226; 1-71.		RT
DR GO; GO:0042025; C:host cell nucleus; IEA.		RT
DR GO; GO:0005634; C:nucleus; IEA.		RT
DR GO; GO:0003723; F:RNA binding; IEA.		RT
DR GO; GO:0003700; F:transcription factor activity; IEA.		RT
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.		RT
DR InterPro; IPR001831; IV_Tat.		RT
DR Pfam; PF00539; Tat; 1.		RT
RESULT 9		RT
040225_9HIV1	PRELIMINARY;	RT
ID 040225_9HIV1	71 AA.	RT
AC 040225;		RT
DT 01-JAN-1998,	integrated into UniProtKB/TrEMBL.	RT
DT 01-JAN-1998, sequence version 1.		RT
DT 07-FEB-2006, entry version 25.		RT
DE Tat protein (Fragment).		RT
GN Name=tat;		RT
OS Human immunodeficiency virus 1.		RT
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;		RT
OC Lentivirus; Primate lentivirus group.		RT
OX NCBI_TAXID=1676;		RT
RN [1]		RT
RP NUCLEOTIDE SEQUENCE.		RT
RC STRAIN=B794_A3ct;		RT
RC MEDLINE=9735179; PubMed=9191845; DOI=10.1006/viro.1997.8586;		RT
RA RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,		RT

PRINTS: PRO0055; HIVATDOMAIN.	DT 01-JAN-1998; sequence version 1.
KW Activator; Nuclear protein; RNA-binding; Transcription;	DT 07-FEB-2006, entry version 25.
KW Transcription regulation.	DE Tat protein (Fragment).
FT NON_TER 71 71	GN Name=rat;
SQ SEQUENCE 71 AA; 8337 MN; 50BB96328495EEA2C CRC64;	OS Human immunodeficiency virus 1.
Query Match Score 11; DB 2; Length 71;	OC Viruses; Retro-transcribing viruses; Orthoretrovirinae;
Best Local Similarity 100.0%; Pred. No. 0.00099;	OC Lentivirus; Primate lentivirus group.
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OX NCB1_TaxID=11676;
Qy 1 YGRKKRKRRR 11	RN [1]
Db 47 YGRKKRKRRR 57	RP NUCLEOTIDE SEQUENCE.
RESULT 11	STRAIN:DJ93-A1cat;
ID Q40227_9HIV1 PRELIMINARY; PRT; 71 AA.	RC MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
AC	RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L., Desrosiers R.C.;
DT 01-JAN-1998, integrated into UniProtKB/T-EMBL.	RA "Activity of human immunodeficiency virus type 1 promoter/TAR regions and tat1 genes derived from individuals with different rates of disease progression." Virology 232:319-331(1997).
DT 01-JAN-1998, sequence version 1.	CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
DT 01-JAN-1998, sequence version 1.	CC
DE Tat protein (Fragment).	CC
GN Name=rat;	DR EMBL; AP000526; AAB62525.1; -; Genomic_DNA.
OS Human immunodeficiency virus 1.	DR HSSP; P04610; 1JFW.
OC Viruses; Retro-transcribing viruses; Orthoretrovirinae;	DR SMR; O40228; 1-71.
Lentivirus; Primate lentivirus group.	DR GO; GO:0043205; C:host cell nucleus; IEA.
OX NCB1_TaxID=11676;	DR GO; GO:0005634; C:nucleus; IEA.
RN [1]	DR PRINTS; PRO003723; F:RNA binding; IEA.
RP NUCLEOTIDE SEQUENCE.	DR DR GO; GO:0003720; F:transcription factor activity; IEA.
RC MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;	DR GO; GO:0006350; P:transcription of transcription, DNA-dependent; IEA.
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L., Desrosiers R.C.;	DR DR InterPro; IPR001831; IV_Tat.
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions and tat1 genes derived from individuals with different rates of disease progression." Virology 232:319-331(1997).	DR Pfam; PF00539; Tat; 1.
RT	DR PRINTS; PRO0055; HIVATDOMAIN.
RT Activator; Nuclear protein; RNA-binding; Transcription;	DR KW Activator; Nuclear protein; RNA-binding; Transcription;
RT Transcription regulation.	DR FT NON_TER 71 71
RL Virology 232:319-331(1997).	DR SQ SEQUENCE 71 AA; 8191 MW; C8800A14AEAFF30E5 CRC64;
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License	Query Match Score 11; DB 2; Length 71;
CC	Best Local Similarity 100.0%; Pred. No. 0.00099;
DR HSSP; P04610; 1JFW.	Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR SMR; O40227_1-71.	Qy 1 YGRKKRKRRR 11
DR GO; GO:0042025; C:host cell nucleus; IEA.	Db 47 YGRKKRKRRR 57
DR GO; GO:0005634; C:nucleus; IEA.	RESULT 13
DR GO; GO:0003723; F:RNA binding; IEA.	040231_9HIV1 PRELIMINARY; PRT; 71 AA.
DR GO; GO:0003700; F:transcription factor activity; IEA.	ID 040231_9HIV1
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.	AC 040231_
DR GO; GO:0005350; P:transcription; IEA.	DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DR GO; GO:0005350; P:transcription; IEA.	DT 01-JAN-1998, sequence version 1.
DR InterPro; IPR001831; IV_Tat.	DT 07-FEB-2006, entry version 25.
DR Pfam; PF00539; Tat; 1.	DE Tat protein (Fragment).
DR PRINTS; PRO0055; HIVATDOMAIN.	GN Name=rat;
DR Activator; Nuclear protein; RNA-binding; Transcription;	OS Human immunodeficiency virus 1.
DR Transcription regulation.	OC Viruses; Retro-transcribing viruses; Orthoretrovirinae;
FT NON_TER 71 71	OC Lentivirus; Primate lentivirus group.
SQ SEQUENCE 71 AA; 8247 MW; C8800B05C90230E5 CRC64;	OX NCB1_TaxID=11676;
Query Match Score 11; DB 2; Length 71;	RP NUCLEOTIDE SEQUENCE.
Best Local Similarity 100.0%; Pred. No. 0.00099;	RC STRAIN:DJ93-A1cat;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
Qy 1 YGRKKRKRRR 11	RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L., Desrosiers R.C.;
Db 47 YGRKKRKRRR 57	RA "Activity of human immunodeficiency virus type 1 promoter/TAR regions and tat1 genes derived from individuals with different rates of disease progression." Virology 232:319-331(1997).
RESULT 12	CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
040228_9HIV1 PRELIMINARY; PRT; 71 AA.	DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
040228_9HIV1 PRELIMINARY; PRT; 71 AA.	AC 040228_9HIV1 PRELIMINARY; PRT; 71 AA.
040228_9HIV1 PRELIMINARY; PRT; 71 AA.	DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.

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CC	EMBL; AF000529; AAB6528.1; -; Genomic_DNA.	Qy	1	YGRKRRQRRR 11							
DR	HSSP; P04610; 1JFW.	Db	47	YGRKRRQRRR 57							
DR	GO; GO:0042025; C:host cell nucleus; IEA.										
DR	GO; GO:0005634; C:nucleus; IEA.										
DR	GO; GO:0003723; F:RNA binding; IEA.										
DR	GO; GO:0003700; F:transcription factor activity; IEA.										
DR	GO; GO:0006155; F:regulation of transcription, DNA-dependent; IEA.										
DR	GO; GO:0006350; F:transcription; IEA.										
DR	InterPro; IPR001831; IV_Tat.										
DR	Pfam; PF00539; Tat; 1.										
DR	PRINTS; PR00055; HIVTARDOMAIN.										
KW	Activator; Nuclear protein; RNA-binding; Transcription;										
KW	Transcription regulation.										
NON_TER	71 AA:	8162 MW:	SAFE3242E82231B3	CRC64;							
SEQUENCE	71 AA:	8162 MW:	SAFE3242E82231B3	CRC64;							
Query Match	55.0%;	Score 11;	DB 2;	Length 71;							
Best Local Similarity	100.0%;	Pred. No. 0.0099;									
Matches	11;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;		
RN	[1]										
RP	NUCLEOTIDE SEQUENCE.										
RC	STRAIN=M984-A3;at;										
RC	O40233_9HIV1 PRELIMINARY; PRT;	71 AA.									
AC	O40233;										
AC	01-JAN-1998; integrated into UniProtKB/TrEMBL.										
DR	Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L., Desrosiers R. C.;										
RA	"Activity of human immunodeficiency virus type 1 promoter/TAR regions and tat1 genes derived from individuals with different rates of disease progression";										
RA	Virology 232:319-331 (1997).										
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms										
CC	Distributed under the Creative Commons Attribution-NoDerivs License										
CC	"Activity of human immunodeficiency virus type 1 promoter/TAR regions and tat1 genes derived from individuals with different rates of disease progression";										
CC	Virology 232:319-331 (1997).										
DR	AF000531; AAB65230.1; -; Genomic_DNA.										
DR	HSSP; P11506; 1TBC.										
DR	SMR; O40233_1-T1.										
DR	GO; GO:042025; C:host cell nucleus; IEA.										
DR	GO; GO:000564; C:nucleus; IEA.										
DR	GO; GO:0003723; F:RNA binding; IEA.										
DR	GO; GO:0003700; F:transcription factor activity; IEA.										
DR	GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.										
DR	GO; GO:0005350; P:transcription; IEA.										
DR	InterPro; IPR001831; IV_Tat.										
DR	PRINTS; PR00055; HIVTARDOMAIN.										
DR	Activator; Nuclear protein; RNA-binding; Transcription;										
KW	"Activity of human immunodeficiency virus type 1 promoter/TAR regions and tat1 genes derived from individuals with different rates of disease progression";										
RN	Virology 232:319-331 (1997).										
RP	NUCLEOTIDE SEQUENCE.										
RX	MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;										
RA	Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L., Desrosiers R. C.;										
RA	"Activity of human immunodeficiency virus type 1 promoter/TAR regions and tat1 genes derived from individuals with different rates of disease progression";										
RA	Virology 232:319-331 (1997).										
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms										
CC	Distributed under the Creative Commons Attribution-NoDerivs License										
CC	"Activity of human immunodeficiency virus type 1 promoter/TAR regions and tat1 genes derived from individuals with different rates of disease progression";										
CC	Virology 232:319-331 (1997).										
DR	AF000530; AAB62529.1; -; Genomic_DNA.										
DR	HSSP; P04610; 1JFW.										
DR	SMR; O40232; 1-T1.										
DR	GO; GO:042025; C:host cell nucleus; IEA.										
DR	GO; GO:0005634; C:nucleus; IEA.										
DR	GO; GO:0003723; F:RNA binding; IEA.										
DR	GO; GO:0003700; F:transcription factor activity; IEA.										
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.										
DR	GO; GO:0006350; P:transcription; IEA.										
DR	InterPro; IPR001831; IV_Tat.										
DR	Pfam; PF00539; Tat; 1.										
DR	PRINTS; PR00055; HIVTARDOMAIN.										
KW	Activator; Nuclear protein; RNA-binding; Transcription;										
KW	Transcription regulation.										
NON_TER	71 AA:	8226 MW:	324F908AF030E216	CRC64;							
SEQUENCE	71 AA:	8226 MW:	324F908AF030E216	CRC64;							
Query Match	55.0%;	Score 11;	DB 2;	Length 71;							
Best Local Similarity	100.0%;	Pred. No. 0.0099;									

Search completed: August 24, 2006, 23:51:26
Job time : 301 secs

Copyright (c) 1993 - 2006 Biocceleration Ltd.
 run on: August 24, 2006, 23:42:38 ; Search time 197 Seconds
 (without alignments)
 46.418 Million cell updates/sec

title: US-10-814-109-2
 perfect score: 20
 sequence: 1 YGRKKRKQRRRKPA\$ADGHR 20

scoring table: OLIGO
 Gapext 60.0 , Gapext 60.0

searched: 2589679 seqs, 457216429 residues

word size : 1

Post-processing: Lifting first 46 summaries

SUMMARIES						
Database :	%					
	Result No.	Score	Query Length	Match DB	ID	Description
A_Genesep_8 : *	1	100.0	20	9	AED21152	SUDAPI-1/
1: genesepGP1990s:*	2	60.0	12	4	AAB31294	Ab823594 BBB peptide
2: genesepGP1990s:*	3	60.0	12	4	AAB31295	Ab823595 BBB peptide
3: genesepGP2000s:*	4	60.0	12	4	AAB31296	Ab823596 BBB peptide
4: genesepGP2000s:*	5	60.0	20	8	AD00689	Ado20689 PSD-95 PD
5: genesepGP2000s:*	6	60.0	20	8	AD00722	Ado20722 PSD-95 PD
6: genesepGP2003bs:*	7	60.0	20	8	AD00723	Ado20723 PSD-95 PD
7: genesepGP2003bs:*	8	60.0	20	8	AD00724	Ado20724 PSD-95 PD
8: genesepGP2004s:*	9	60.0	20	8	AD020599	Ado20599 NMDA receptor peptide
9: genesepGP2005s:*	10	60.0	20	8	AD020674	Ado20674 PSD-95 PD
10: genesepGP2006s:*	11	60.0	20	8	AD020697	Ado20697 PSD-95 PD
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						

DECIT 8 1

```

RESULT 1
AED21152
ID AED21152 standard; peptide ; 20 AA.
XX
AC AED21152;
XX
DT 01-DEC-2005 (first entry)
XX
DE SUDAPI-1/ HIV Tat domain fusion peptide, TSUDAPI-1 SEQ ID NO: 2.

```

XX	KW	Protein interaction; therapeutic; cerebrovascular ischemia;
	KW	cerebroprotective; vasoprotic; hypoxia; ischemia; multiple sclerosis;
	KW	neuroprotective; Huntington's chorea; anticonvulsant; nootropic;
	KW	Parkinson's disease; anti-parkinsonian; Alzheimer's disease; hyperglycemia;
	KW	antidiabetic; diabetes; trauma; tranquilizer; pulmonary; epilepsy;
	KW	grand mal seizure; muscle hypertension; muscle relaxant; paralysis;
	KW	macular degeneration; asthma; anti-tachamic; cardiac arrest; cardiac;
	KW	neuroleptic; schizophrenia; AIDS dementia complex; dementia;
	KW	inflammation; anti-inflammatory; pain; analgesic; opiate dependence;
	KW	anti-addictive; cocaine addiction; alcoholism; anti-alcoholic;
	KW	anorexia nervosa; anabolic; eating-disorders; gen.;
	KW	etc.

SLC-unique domain anchoring protein inhibitor.			
Key	Value	Location/Qualifiers	Notes
XX	SLC-unique domain anchoring protein inhibitor.		
XX	Homo sapiens.		
OS	Human immunodeficiency virus.		
XX			
FH	Key	1..11	
FT	Region	/note= "HIV transduction domain (TAT)"	
FT	Region	12..20	
FT	Region	/note= "Src unique domain anchoring protein inhibitor 1"	
FT			

XX US2005222042-A1.
XX PN
XX PD 06-OCT-2005.
PF 30-MAR-2004; 2004US-00814109.
XX PR 30-MAR-2004; 2004US-00814109.
XX PA (HOSP-) HOSPITAL FOR SICK CHILDREN RES INST.
XX PI Salter MW, Gingrich JR;
XX DD 2005 CONCERN /71

Modifying N-methyl-D-aspartate receptor interaction with non-receptor tyrosine kinase Src in cells, comprises administering composition comprising Src-unique domains anchoring protein inhibitor to cells.

Claim 13; SEQ ID NO 2; 32pp; English.

The present invention provides a method for modifying N-methyl-D-aspartate receptor (NMDAR) interaction with non-receptor tyrosine kinase Src in cells. The method involves administering a composition including at least one Src-unique domain anchoring protein inhibitor (SUDAPI) to the cells, where modification ameliorates a disease or condition related to NMDAR signaling. Diseases or conditions ameliorated by the invention include stroke, hypoxia, ischemia, multiple sclerosis, Huntington's chorea, Parkinson's disease, Alzheimer's disease, hyperglycemia, diabetes, traumatic injury, epilepsy, grand mal seizures, spasticity, cerebral palsy, asthma, cardiac arrest, macular degeneration, mental diseases, schizophrenia, AIDS dementia complex, other dementias, AIDS wasting syndrome, inflammation, pain, opioid addiction, cocaine addiction, alcohol addiction and other conditions associated with substance abuse and anorexia. The present sequence is the SUDAPI-1/HIV Tat domain fusion peptide, TSUDAPI-1.

pulmonary or blood components to form a stable covalent bond, were the therapeutic agent may be a peptide. Pulmonary drug delivery is useful as it increases the drug re-uptake time in the lungs and reduces the risk of extrapharmacological side effects. Modified therapeutic agents of this type may be anti-histamines, anti-arginine, anti-hypertensive or anti-arrhythmic agents, anti-depressants, bronchodilators, opioids or their analogues, anti-inflammatory agents, or anti-thyroid deficiency agents. The present sequence is a BBB peptide

Unidentified.	OS XX PN XX	PA XX PI XX	(ARBO-) ARBOR VITA CORP.
WO2004045535-A2.	XX	Lu PS, Garman JD, Belmares MP;	
03-JUN-2004.	DR WPI : 2004-420526/39.		
14-NOV-2003; 2003WO-US036698.	XX		
14-NOV-2002; 2002US-0426212P.	PT PR XX		
14-NOV-2002; 2002US-0426213P.	PT PR XX		
PA	PS	Example 3 ; Page 97 ; 146bp; English.	
XX	XX	The invention describes a pharmaceutical composition comprising an isolated, recombinant or synthetic polypeptide that inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein and a carrier, diluent or excipient and that comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala. Also described are: an isolated, recombinant or synthetic polypeptide for use in therapy and that comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala and a protein; and a method for determining whether a test compound inhibits binding between a PDZ protein and a N-methyl-D-aspartate (NMDA) receptor.	
XX	CC	The pharmaceutical composition is useful in treating a neuronal disorder, which is an injury caused by stroke or ischaemia. This is the amino acid sequence of a polypeptide that can inhibit the interaction between NMDA and PDZ domain containing protein PSD-95.	
XX	CC	Sequence 20 AA;	
XX	CC	Query Match 60.0%; Score 12; DB 8; Length 20; Best Local Similarity 100.0%; Pred. No. 0.00022; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
XX	CC	Qy 1 YGRKKEQRQQRK 12 Db 1 YGRKKEQRQQRK 12	
XX	CC	Sequence 20 AA;	
XX	CC	Sequence 20 AA;	

```

Query Match      60.0%; Score 12; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0
1 YGRRKKRQRKK 12
1 YGRRKKRQRKK 12

```

RESULT 7
 D ADO20599 standard; peptide; 20 aa.
 X
 C ADO20599;
 X
 T 26-AUG-2004 (first entry)
 X NMDA receptor PSD-95 binding inhibitor peptide #4.
 X Neuroprotective; Gene therapy; N-methyl-D-aspartate receptor;
 X NMDA receptor; PDZ domain; PDZ protein; binding inhibitor;
 X
 X
 X

DB	PSD-95 PDZ domain binding peptide #6.
XX	
KW	neuroprotective; gene therapy; N-methyl-D-aspartate receptor;
KW	NMDA receptor; PDZ domain; PDZ protein; binding inhibitor;
KW	neuronal disorder; stroke; ischaemia; PSD-95; PDZ domain.
XX	
OS	Unidentified.
XX	

PN WO2004045535-A2.
 XX
 PD 03 - JUN - 2004 .
 XX
 PF 14 - NOV - 2003 ; 2003WO-US036698 .
 XX
 PR 14 - NOV - 2002 ; 2002US - 0426212P .
 PR 14 - NOV - 2002 ; 2002US - 0426213P .
 XX (ARBO-) ARBOR VITA CORP .
 PA
 PI Lu PS , Garman JD , Belmares MP ;
 XX DR WPI ; 2004-420526/39 .
 XX PT New pharmaceutical composition comprising a polypeptide that inhibits
 PT binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein .

PT useful in treating a neuronal disorder e.g. an injury caused by stroke or ischaemia.

XX Example 9; Page 104; 146pp; English.

The invention describes a pharmaceutical composition comprising an isolated, recombinant or synthetic polypeptide that inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein and a carrier, diluent or excipient and that comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala. Also described are: an isolated, recombinant or synthetic polypeptide for use in therapy and that comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala and inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein; and a method for determining whether a test compound inhibits binding between a PDZ protein and a N-methyl-D-aspartate (NMDA) receptor.

The pharmaceutical composition is useful in treating a neuronal disorder, which is an injury caused by stroke or ischaemia. This is the amino acid sequence of a PDZ domain ligand that binds to the PDZ domain of PSD-95. Sequence 20 AA;

Query Match 60.0%; Score 12; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ
Y 1 YGRKKRKQRKK 12
D 1 YGRKKRKQRKK 12

RESULT 9
ADO2097
ID ADO2097 standard; peptide; 20 AA.
AC ADO2097;
XX DT 26-AUG-2004 (First entry)
DB PSD-95 PDZ domain binding peptide #39.
XX

KW neuroprotective; gene therapy; N-methyl-D-aspartate receptor;
KW NMDA receptor; PDZ domain; binding inhibitor;
KW neuronal disorder; stroke; ischaemia; PSD-95; PDZ domain.
OS Unidentified.
XX DR 03-JUN-2004.
XX PN WO2004045535-A2.
XX PD 03-JUN-2004.
XX PF 14-NOV-2003; 2003WO-US036698.
XX PR 14-NOV-2002; 2002US-0426212P.
XX PR 14-NOV-2002; 2002US-0426213P.
XX PA (ARBO-) ARBOR VITA CORP.
XX PI Lu PS, Garman JD, Belmares MP;
XX DR 2004-420526/39.
XX PT New pharmaceutical composition comprising a polypeptide that inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein, useful in treating a neuronal disorder e.g. an injury caused by stroke or ischaemia.

XX PT 14-NOV-2003; 2003WO-US036698.
XX PR 14-NOV-2002; 2002US-0426212P.
XX PR 14-NOV-2002; 2002US-0426213P.
XX PA (ARBO-) ARBOR VITA CORP.
XX PI Lu PS, Garman JD, Belmares MP;
XX DR 2004-420526/39.

XX PT New pharmaceutical composition comprising a polypeptide that inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein, useful in treating a neuronal disorder e.g. an injury caused by stroke or ischaemia.
XX PS Example 9; Page 105; 146pp; English.
XX The invention describes a pharmaceutical composition comprising an isolated, recombinant or synthetic polypeptide that inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein and a carrier, diluent or excipient and that comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala. Also described are: an isolated, recombinant or synthetic polypeptide for use in therapy and that comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala and inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein; and a method for determining whether a test compound inhibits binding between a PDZ protein and a N-methyl-D-aspartate (NMDA) receptor. The pharmaceutical composition is useful in treating a neuronal disorder, which is an injury caused by stroke or ischaemia. This is the amino acid sequence of a PDZ domain ligand that binds to the PDZ domain of PSD-95. Sequence 20 AA;

CC recombinant or synthetic polypeptide for use in therapy and that comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala and inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein; and a method for determining whether a test compound inhibits binding between a PDZ protein and a N-methyl-D-aspartate (NMDA) receptor. The pharmaceutical composition is useful in treating a neuronal disorder, which is an injury caused by stroke or ischaemia. This is the amino acid sequence of a PDZ domain ligand that binds to the PDZ domain of PSD-95. Sequence 20 AA;

Query Match 60.0%; Score 12; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ
Y 1 YGRKKRKQRKK 12
D 1 YGRKKRKQRKK 12

RESULT 10
ADO20730
ID ADO20730 standard; peptide; 20 AA.
XX AC ADO20730;
XX DT 26-AUG-2004 (First entry)
XX XX PSD-95 PDZ domain binding peptide #72.
XX DE XX
XX KW neuroprotective; gene therapy; N-methyl-D-aspartate receptor;
KW NMDA receptor; PDZ protein; binding inhibitor;
KW neuronal disorder; stroke; ischaemia; PSD-95; PDZ domain.
OS Unidentified.
XX XX
XX PN WO2004045535-A2.
XX PD 03-JUN-2004.
XX XX
XX PN WO2004045535-A2.
XX PD 03-JUN-2004.
XX PF 14-NOV-2003; 2003WO-US036698.
XX PR 14-NOV-2002; 2002US-0426212P.
XX PR 14-NOV-2002; 2002US-0426213P.
XX PA (ARBO-) ARBOR VITA CORP.
XX PI Lu PS, Garman JD, Belmares MP;
XX DR 2004-420526/39.
XX PT New pharmaceutical composition comprising a polypeptide that inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein, useful in treating a neuronal disorder e.g. an injury caused by stroke or ischaemia.

XX PS Example 9; Page 105; 146pp; English.

XX The invention describes a pharmaceutical composition comprising an isolated, recombinant or synthetic polypeptide that inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein and a carrier, diluent or excipient and that comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala and inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein; and a method for determining whether a test compound inhibits binding between a PDZ protein and a N-methyl-D-aspartate (NMDA) receptor. The pharmaceutical composition is useful in treating a neuronal disorder, which is an injury caused by stroke or ischaemia. This is the amino acid sequence of a PDZ domain ligand that binds to the PDZ domain of PSD-95. Sequence 20 AA;

channel, proteins or cellular protein interaction domains that effect the CC TRP channel protein interactions) and determining whether a test compound CC modulates binding between a TRP channel protein and a PDZ domain- CC containing polypeptide (comprising contacting a TRP channel protein and a PDZ domain-containing polypeptide, and measuring the CC sequence with a PDZ domain-containing polypeptide, and measuring the CC amount of complex formed between the TRP channel PDZ-Ligand sequence and CC the PDZ domain-containing polypeptide). The TRP-associated protein in the CC inhibitor cited above comprises at least one PDZ domain selected from RIM CC -2, Mint 1, INADL, Syntriphin 1 alpha, SITAC-18, LIM mystique, 20-1, PAR3L, MAST2, PARS, and novel serine protease. The TRP channel protein is CC human TRPM7 or mouse TRPM7. The methods and compositions of the present CC invention are useful for reducing the damaging effect of an injury to CC mammalian cells, including brain and spinal cord cells, by treatment with CC compounds which reduce cell death or dysfunction, including cellular CC damage following episodes of tissue ischemia and trauma. Also treatable CC with the methods and compositions and acute or chronic degeneration, such CC as in stroke, epilepsy, Parkinson's disease, glaucoma, Alzheimer's CC disease, spinal cord injuries, myocardial ischemia, Huntington's chorea, CC inherited ataxias and motor neuron disease. The present sequence is a CC peptide tested for its ability to bind to a selected PDZ domain or CC inhibit the binding of the PDZ domain to a TRP protein.

XX Sequence 20 AA;

Query Match	60.0%	Score 12;	DB 9;	Length 20;
Best Local Similarity	100.0%	Pred. No.	0.00022;	
Matches 12;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

Qy 1 YGRKKRKQRQQRK 12
Db 1 YGRKKRKQRQQRK 12

RESULT 13
AEB07972
ID AEB07972 standard; peptide; 20 AA.
XX AC AEB07972;
XX DT 08-SEP-2005 (first entry)
XX DE Peptide binding to RIM2 PDZ domain 1 SEQ ID 364.

KW Protein interaction; protein therapy; TRP; cell death; PDZ domain;
KW transient receptor potential channel; TRP; cell death; PDZ domain;
KW Vasotropin; Nootropic; Neuroprotective; Ophthalmological;
KW Antiparkinsonian; Anticonvulsant; cerebroprotective; pulmonary; cardiant;
KW muscular-gen.; CNS-gen.; brain injury; spinal cord injury; ischemia;
KW trauma; degeneration; cerebrovascular ischemia; epilepsy;
KW Parkinson's disease; glaucoma; Alzheimer's disease; myocardial ischemia;
KW Huntington's chorea; ataxia; motor neuron disease.
XX OS Synthetic.
XX PN WO2005061548-A1.
XX PD 07-JUL-2005.
XX XX 22-DEC-2004; 2004WO-CA002193.
XX PR 23-DEC-2003; 2003US-0532169P.
XX PA (ARBO-) ARBOR VITA CORP.
PA (NONO-) NONO INC.
XX PI Tymianski M, Garman JD, Belmares MP;
XX DR 2005-479449/48.
XX PT New isolated polypeptides inhibiting binding between a transient receptor potential (TRP) channel protein and a TRP-associated protein, useful in reducing damage to mammalian cells following stroke, epilepsy or spinal cord injuries.

XX Example 3; SEQ ID NO 364; 377bp; English.
PS The invention relates to an inhibitor comprising an isolated, recombinant
XX CC or synthetic polypeptide that inhibits binding between a transient
CC receptor potential (TRP) channel protein and a TRP-associated protein
CC (e.g. one containing a PDZ domain). Also included are a pharmaceutical
CC composition comprising the inhibitor cited above (and a physiological
CC carrier, diluent or excipient), an inhibitor comprising a nucleic acid
CC sequence capable of inhibiting the expression of a TRP channel protein
CC post transcriptionally, treating mammalian cell injury (comprising
CC introducing a modulator of binding between a TRP channel protein and a
CC TRP channel associated protein into a cell), reducing the damaging effect
CC of ischemia/trumatic injury to the brain/spinal cord in a mammal
CC (comprising treating the mammal with a non-toxic, damage-reducing,
CC effective amount of a modulator of binding between a TRP channel protein
CC and a TRP channel associated protein), controlling the concentration of
CC Ca²⁺-dependent signaling molecules in the vicinity of ion channel pores
CC of cells in vivo (to prevent the diffusion of toxic amounts of the Ca²⁺-
CC influx) to prevent the triggering of neurotoxic phenomena (comprising
CC administering an effective, non-toxic amount of a modulator of TRP
CC channel proteins or cellular protein interaction domains that effect the
CC TRP channel protein interactions) and determining whether a test compound
CC modulates binding between a TRP channel protein and a PDZ domain-
CC containing polypeptide (comprising contacting a TRP channel PDZ-ligand
CC sequence with a PDZ domain-containing polypeptide, and measuring the
CC amount of complex formed between the TRP channel PDZ-ligand sequence and
CC the PDZ domain-containing polypeptide). The TRP-associated protein in the
CC inhibitor cited above comprises at least one PDZ domain selected from RIM
CC -2, Mint 1, INADL, Syntriphin 1 alpha, SITAC-18, LIM mystique, 20-1,
CC PAR3L, MAST2, PARS, and novel serine protease. The TRP channel protein is
CC human TRPM7 or mouse TRPM7. The methods and compositions of the present
CC invention are useful for reducing the damaging effect of an injury to
CC mammalian cells, including brain and spinal cord cells, by treatment with
CC compounds which reduce cell death or dysfunction, including cellular
CC damage following episodes of tissue ischemia and trauma. Also treatable
CC with the methods and compositions and acute or chronic degeneration, such
CC as in stroke, epilepsy, Parkinson's disease, glaucoma, Alzheimer's
CC disease, spinal cord injuries, myocardial ischemia, Huntington's chorea,
CC peptide tested for its ability to bind to a selected PDZ domain or
CC inhibit the binding of the PDZ domain to a TRP protein.

XX SQ Sequence 20 AA;

Query Match 60.0%; Score 12; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRKQRQQRK 12
Db 1 YGRKKRKQRQQRK 12

RESULT 14
AEB07884
ID AEB07884 standard; peptide; 20 AA.
XX AC AEB07884;
XX DT 08-SEP-2005 (first entry)
XX XX Peptide inhibitor of TRPM7-ZO-1/INADL PDZ domains, 1852.
KW Protein interaction; protein therapy;
KW transient receptor potential channel; TRP; cell death; PDZ domain;
KW Vasotropin; Nootropic; Neuroprotective; Ophthalmological;
KW Antiparkinsonian; Anticonvulsant; cerebroprotective; pulmonary; cardiant;
KW muscular-gen.; CNS-gen.; brain injury; spinal cord injury; ischemia;
KW trauma; degeneration; cerebrovascular ischemia; epilepsy;
KW Parkinson's disease; glaucoma; Alzheimer's disease; myocardial ischemia;
KW Huntington's chorea; ataxia; motor neuron disease.

OS Synthetic.
 XX WO2005061548-A1.
 PN XX RESULT 15
 PD XX AAW50263 standard; protein; 11 AA.
 XX ID AAW50263
 XX AC AAW50263;
 XX DT 17-OCT-2003 (revised)
 PR XX DT 20-JUL-1998 (first entry)
 XX HIV-1 tat protein.

XX Mouse; BH3 interacting domain death agonist; BID; BCL-2 family;
 KW apoptosis; regulation; cell death; inflammation; cancer; arthritis;
 KW autoimmune disease; viral infection; lymphoproliferative.
 XX HIV-1 tat protein.

XX Human immunodeficiency virus 1.
 OS XX WO9809980-A1.
 PN XX
 PR XX
 DR XX
 WPI; 2005-479449/48.
 XX
 PR New isolated polypeptides inhibiting binding between a transient receptor
 PR potential (TRP) channel protein and a TRP-associated protein, useful in
 PR reducing damage to mammalian cells following stroke, epilepsy or spinal
 PR cord injuries.
 PR XX
 PS XX Example 3; SEQ ID NO 276; 377pp; English.
 XX
 CC The invention relates to an inhibitor comprising an isolated, recombinant
 CC or synthetic polypeptide that inhibits binding between a transient
 CC receptor potential (TRP) channel protein and a TRP-associated protein
 CC (e.g. one containing a PDZ domain). Also included are a pharmaceutical
 CC composition comprising the inhibitor cited above (and a physiologically
 CC compatible, diluent or excipient), an inhibitor comprising a nucleic acid
 CC sequence capable of inhibiting the expression of a TRP channel protein
 CC post transcriptionally, treating mammalian cell injury (comprising
 CC introducing a modulator of binding between a TRP channel protein and a
 CC TRP channel associated protein in a cell), reducing the damaging effect
 CC of ischaemia/traumatic injury to the brain/spinal cord in a mammal
 CC comprising treating the mammal with non-toxic, damage-reducing,
 CC effective amount of a modulator of binding between a TRP channel protein
 CC and a TRP channel associated protein, controlling the concentration of
 CC Ca²⁺-dependent signalling molecules in the vicinity of ion channel pores
 CC of cells in vivo (to prevent the diffusion of toxic amounts of the
 CC Ca²⁺ influx), to prevent the triggering of neurotoxic phenomena (comprising
 CC administering an effective non-toxic amount of a modulator of TRP
 CC channel proteins or cellular protein interaction domains that effect the
 CC TRP channel protein interactions) and determining whether a test compound
 CC modulates binding between a TRP channel protein and a PDZ domain
 CC containing polypeptide (comprising contacting a TRP channel PDZ-Ligand
 CC sequence with a PDZ domain-containing polypeptide, and measuring the
 CC amount of complex formed between the TRP channel PDZ-Ligand sequence and
 CC the PDZ domain-containing polypeptide). The TRP-associated protein in the
 CC inhibitor cited above comprises at least one PDZ domain selected from RIM
 CC -2, Mapt, 1, INAD, Syntrphin 1, alpha, STAC-1B, LIM myctine, ZO-1,
 CC PAR3L, MAST2, PARS, and novel serine procase. The TRP channel protein is
 CC human TRPM7 or mouse TRPM7. The methods and compositions of the present
 CC invention are useful for reducing the damaging effect of an injury to
 CC mammalian cells, including brain and spinal cord cells, by treatment with
 CC compounds which reduce cell death or dysfunction, including cellular
 CC damage following episodes of tissue ischaemia and trauma. Also treatable
 CC with the methods and compositions and acute or chronic degeneration, such
 CC as in stroke, epilepsy, Parkinson's disease, glaucoma, Alzheimer's
 CC disease, spinal cord injuries, myocardial ischaemia, Huntington's chorea,
 CC inherited ataxias and motor neurone disease. The present sequence is a
 CC peptide tested for its ability to bind to a selected PDZ domain or
 CC inhibit the binding of the PDZ domain to a TRP protein.
 XX Sequence 20 AA:
 SQ

Query Match 60.0%; Score 12; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.00022;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKGRQRQRK 12
 Db 1 YGRKGRQRQRK 12

Search completed: August 24, 2006, 23:46:23
 Job time : 200 secs

DE Tat protein.	PFam; PF00539; Tat; 1.
GN Name=tat;	DR PRINTS; PRO0055; HIVTDOMAIN.
OS Human immunodeficiency virus 1.	DR Activator; Nuclear protein; RNA-binding; Transcription;
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;	KW Transcription regulation.
OC Lentivirus; Primate lentivirus group.	KW
OX NCBI_TaxID=11676;	SEQUENCE 101 AA; 11408 MW; 9D1E270E0E1E5A0F CRC64;
RN [1]	Query Match 74.8%; Score 80; DB 2; Length 101;
NUCLEOTIDE SEQUENCE.	Best Local Similarity 70.0%; Pred. No. 0.00064;
RC STRAIN=03ZAK098B1;	Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
RA Birditt B.A., Rousseau C.M., Korber B.T., Goulder P., Brander C.,	RP
RA Kiepiela P., Walker B.D., Mullins J.I.;	Qy 1 YGRKKRKRRRKPKASADGHR 20
RT "HIV HLA epitope mapping from Durban, South Africa.";	Db 47 YGRKKRKRRRKPKASADGHR 66
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.	CC
CC Copyright by the UniProt Consortium, see http://www.uniprot.org/terms	RESULT 4
CC Distributed under the Creative Commons Attribution-NoDerivs License	OBU520_9HIV1
CC	ID OBU520_9HIV1 PRELIMINARY; PRT; 101 AA.
DR EMBL; A878061; AWM8119_1; Genomic RNA.	AC OBU520;
DR GO; GO:0042025; C:host cell nucleus; IEA.	DT 01-MAR-2002; integrated into UniProtKB/TREMBL.
DR GO; GO:005634; C:nucleus; IEA.	DT 01-MAR-2002; sequence version 1.
DR GO; GO:0003723; F:RNA binding; IEA.	DT 01-FEB-2006; entry version 17.
DR GO; GO:0003700; F:transcription factor activity; IEA.	DE Tat protein.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.	GN Name=tat;
DR GO; GO:0006350; P:transcription; IEA.	OS Human immunodeficiency virus 1.
DR InterPro; IPR01831; IV_Tat.	OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
DR PFam; PF00539; Tat; 1.	OC Lentivirus; Primate lentivirus group.
DR PRINTS; PRO0055; HIVTDOMAIN.	OX NCBI_TaxID=11676;
Activator; Nuclear protein; RNA-binding; Transcription;	RP NUCLEOTIDE SEQUENCE.
Transcription regulation.	RX MEDLINE=2198875; PubMed=11991972;
SEQUENCE 101 AA; 11532 MW; 230D1C1CDC6E5CDD CRC64;	RX DOI=10.1128/JVI.76.11.5435-5451.2002;
Qy 1 YGRKKRKRRRKPKASADGHR 20	RA Novitsky V., Smith U.R., Gilbert P., McLane M.F., Chigwedere P.,
Db 47 YGRKKRKRRRKPKASADGHR 66	RA Williamson C., Ndung'u T., Klein I., Chang S.-Y., Peter T., Thior I.,
CC	RA Foley B.T., GaoIekwe S., Rybak N., Gaseitsiwe S., Vannberg F.,
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	RA Marlink R., Lee T.-H., Essex M.,
CC Distributed under the Creative Commons Attribution-NoDerivs License	RT Human immunodeficiency virus type 1 subtype C molecular phylogeny:
CC	RT consensus sequence for an AIDS vaccine design?";
CC	RL J. Virol. 76:5435-5451 (2002).
CC	RN NUCLEOTIDE SEQUENCE.
CC	RA Novitsky V.A., McLane M.F., Chigwedere P., Ndung'u T., Klein I.,
CC	RA Chang S.-Y., Peter T., Thior I., Rybak N., Gaseitsiwe S., Vannberg F.,
CC	RA Marlink R., Lee T.-H., Essex M.,
CC	RA Foley B.T., GaoIekwe S., Rybak N., Gaseitsiwe S., Vannberg F.,
CC	RA Marlink R., Lee T.-H., Essex M.,
CC	RA "Human immunodeficiency virus type 1 subtype C molecular phylogeny:
CC	RL J. Virol. 76:5435-5451 (2002).
CC	RN DR AF443108; AAL34859.1; -; Genomic_DNA.
CC	DR HSP; P12506; 1TBC.
CC	DR GO; GO:0042025; C:host cell nucleus; IEA.
CC	DR GO; GO:005634; C:nucleus; IEA.
CC	DR GO; GO:0003723; F:RNA binding; IEA.
CC	DR GO; GO:0003700; F:transcription factor activity; IEA.
CC	DR GO; GO:0006355; P:transcription, DNA-dependent; IEA.
CC	DR InterPro; IPR01831; IV_Tat.
CC	DR PRINTS; PRO0055; HIVTDOMAIN.
CC	DR Activator; Nuclear protein; RNA-binding; Transcription;
CC	KW Transcription regulation.
CC	SQ SEQUENCE 101 AA; 11500 MW; 5E7E8AC7AD25767 CRC64;
CC	Query Match 74.8%; Score 80; DB 2; Length 101;
CC	Best Local Similarity 70.0%; Pred. No. 0.00064;
CC	Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
CC	RP
CC	Qy 1 YGRKKRKRRRKPKASADGHR 20
CC	Db 47 YGRKKRKRRRKPKASADGHR 66
CC	CC
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CC	CC
CC	EMBL; AY622547; ATT76859.1; -; Genomic_DNA.
CC	DR SMR; Q6B44; 1-86.
CC	DR GO; GO:0042025; C:host cell nucleus; IEA.
CC	DR GO; GO:005634; C:nucleus; IEA.
CC	DR GO; GO:0003723; F:RNA binding; IEA.
CC	DR GO; GO:0003700; F:transcription factor activity; IEA.
CC	DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
CC	DR InterPro; IPR001831; IV_Tat.

RESULT 5				
Q355P9_9HIV1	PRELIMINARY;	PRT;	101 AA.	
ID O355P9_				
AC Q355P9_				
DR 11-OCT-2005, integrated into UniProtKB/TremBL.				
DR 11-OCT-2005, sequence version 1.				
DR 07-FEB-2006, entry version 4.				
DE Rat protein.				
GN Name=tat;				
OS Human immunodeficiency virus 1.				
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;				
OC Lentivirus; Primate lentivirus group.				
OX NCBI_TaxID:11676;				
RN [1]				
RP NUCLEOTIDE SEQUENCE.				
RC STRAIN=04ZAS16IB1;				
RA Birditt B.A., Rousseau C.M., Korber B.T., Goulder P., Brander C.,				
RA Klepela P., Walker B.D., Mullins J.I.,				
RT "HIV HLA epitope mapping from Durban, South Africa.";				
RL Submitted (AUG-2005) to the EMBL/Genbank/DDBJ databases.				
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CC				
DR EMBL; DOI:164115; ANZ91841_1; Genomic RNA.				
DR GO:GO:0042025; C:host cell nucleus; IEA.				
DR GO:GO:0005634; C:nucleus; IEA.				
DR GO:GO:0003223; P:RNA binding; IEA.				
DR GO:GO:0003700; P:transcription factor activity; IEA.				
DR GO:GO:0006355; P:regulation of transcription, DNA-dependent; IEA.				
DR GO:GO:0006350; P:transcription; IEA.				
DR InterPro; IPR01831; IV_Rat				
DR Pfam; PF00539; Tat_1.				
DR PRINTS; PR00055; HIVATDOMAIN.				
KW Activator; Nuclear protein; RNA-binding; Transcription;				
KW Transcription regulation.				
SQ SEQUENCE 101 AA; 11459 MW; 79E2BB916116356F CRC64;				
Query Match 73.8%; Score 79; DB 2; Length 101;				
Best Local Similarity 70.0%; Pred: No. 0.00089;				
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;				
Qy 1 YGRKKRQRRKPKASADGHR 20				
Db 47 YGRKKRQRRKPKASSEHQ 66				
RESULT 6				
Q6X6HO_9HIV1	PRELIMINARY;	PRT;	101 AA.	
ID Q6X6HO_				
AC Q6X6HO_				
DR 05-JUL-2004, integrated into UniProtKB/TremBL.				
DR 05-JUL-2004, sequence version 1.				
DR 07-FEB-2006, entry version 10.				
DE Tat protein.				
GN Name=tat;				
OS Human immunodeficiency virus 1.				
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;				
OC Lentivirus; Primate lentivirus group.				
OX NCBI_TaxID:11676;				
RN [1]				
RP NUCLEOTIDE SEQUENCE.				
PubMed=10320594; DOI=10.1089/08892204172535;				
RA Arroyo M.A., Hoelscher M., Sanders-Buell E., Herlinger K.H., Samky E.,				
RA Maboko L., Hoffmann O., Robb M.R., Blix D.L., McCutchan F.E.,				
RT "HIV Type 1 Subtypes among Blood Donors in the Mbeya Region of				
RT Southwest Tanzania"; AIDS Res. Hum. Retroviruses 20:895-901 (2004).				
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DR EMBL; AV253322; AQ98283.1; -; Genomic_DNA.				
RESULT 8				
Q900L1_9HIV1	PRELIMINARY;	PRT;	101 AA.	
ID Q900L1_				
AC Q900L1_				

ID Q8ATV7_9HIV1 PRELIMINARY; PRT; 71 AA.
AC Q8ATV7; UniProtKB/TREMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Tat protein (Fragment).
Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nanteza M.B., Yirell D.L., Kintu P., Kaleebu P., Biryuhahwo B.,
RA Morgan D., Whitworth J.; Submitted (Oct-2001) to the EMBL/GenBank/DDBJ databases.
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CC EMBL; AF425965; AN31625.1; -; Genomic DNA.
DR HSSP; P04613; 1K5P.
SMR; Q8ATV7; 1-71.
DR GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; RNA binding; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR01831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTARDOMAIN.
Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 71
SQ SEQUENCE 71 AA; 8243 MW; 3D10B9A460729AF2 CRC64;

Query Match, Score 78%; DB 2; Length 71;
 Best Local Similarity 70.0%; Pred. No. 0.00087; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 4; Gaps 0;
 Name=tat;

Qy 1 YGRKKRRRKPSADGHR 20
 DR 47 YGRKKRRRKARRPSQQHQ 66

DB 47 YGRKKRRRKARRPSQQHQ 66

RESULT 12
Q8BMM5_9HIV1 PRELIMINARY; PRT; 72 AA.
ID Q8BMM5; UniProtKB/TREMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Tat protein (Fragment).
Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ranga U., Nagendran R., Siddappa N.B., Mahadevan A., Parthasarathy S.,
RA Shankar S.K.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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CC EMBL; AY064236; AAL51174.1; -; Genomic_DNA.
DR HSSP; P12506; 1TB.C.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR01831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTARDOMAIN.
Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 72
SQ SEQUENCE 72 AA; 8385 MW; 656790CF4999FB3B CRC64;

Query Match, Score 78%; DB 2; Length 72;
 Best Local Similarity 70.0%; Pred. No. 0.00088; Indels 3; Gaps 0;
 Mismatches 14; Conservative 3; Gaps 0;
 Name=tat;

Qy 1 YGRKKRRRKPSADGHR 20
 DR 47 YGRKKRRRKARRPSQQHQ 66

DB 47 YGRKKRRRKARRPSQQHQ 66

RESULT 14
Q8BMM7_9HIV1 PRELIMINARY; PRT; 72 AA.
ID Q8BMM7; UniProtKB/TREMBL.
AC Q8BMM7;
DT 01-MAR-2002, integrated into UniProtKB/TREMBL.
DT 01-MAR-2002, sequence version 1.

DT 07-FEB-2006, entry version 16.
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentiviruses; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE;
RA Ranga U., Nagendran R., Siddappa N.B., Mahadevan A., Parthasarathy S.,
RA Shankar S.K.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; AY064235; AL51173.1; -; Genomic_DNA.
DR HSSP; P12506; ITBC.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:005634; C:nucleus; IEA.
DR GO; GO:000722; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:000350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR0005; HIV1DOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA; 8428 MW; 13BCE610D7B0062B CRC64;
Query Match 72.9%; Score 78; DB 2; Length 72;
Best Local Similarity 70.0%; Pred. No. 0.00088;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db 47 YGRKERRQRKPA\$ADGHR 20
Db 47 YGRKERRQRKPA\$Q\$EDHQ 66

RESULT 15
Q8UWMB8_9HIV1 ID Q8UWMB8_9HIV1 PRELIMINARY; PRT; 72 AA.
AC Q8UWMB8;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DB Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentiviruses; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE;
RA Ranga U., Nagendran R., Siddappa N.B., Mahadevan A., Parthasarathy S.,
RA Shankar S.K.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; AY064234; AL51172.1; -; Genomic_DNA.
DR HSSP; P12506; ITBC.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:005634; C:nucleus; IEA.
DR GO; GO:000723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:000350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.

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OM protein - protein search, using sw model

Run on: August 24, 2006, 23:32:41 ; Search time 39 Seconds
 (without alignments)
 49.342 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 107

Sequence: 1 YGRKKBQRQQRKPAASADGHR 20

Scoring table: BloSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0^{*}

Maximum Match 10^{*}

Listing first 45 summaries

Database : PIR_80;*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	71.0	71	2 T09384	trans-activating t
2	71	66.4	86	2 A25700	trans-activating t
3	71	66.4	86	2 S33982	trans-activating t
4	71	66.4	95	1 TNLJ12	trans-activating t
5	71	66.4	101	1 E44001	trans-activating t
6	71	66.4	101	1 T09446	tat protein - human
7	70	65.4	87	2 T01665	tat protein - human
8	67	62.6	86	1 TNLJND	trans-activating t
9	64	59.8	72	1 TNLJH4	trans-activating t
10	62	57.9	86	2 TNLJZR	trans-activating t
11	62	57.9	86	2 JC5591	transactivator protein
12	62	57.9	86	2 S54381	protein - human
13	53	49.5	953	2 B70681	probable rne prote
14	50	46.7	371	2 S39625	T-cell receptor al
15	50	46.7	399	2 A39625	unknown protein TS
16	50	46.7	421	2 C96806	protein-tyrosine k
17	50	46.7	541	1 A43610	probable membrane
18	50	46.7	542	1 TVHUSC	T-cell-specific tr
19	49	45.8	37	2 S29829	T-cell-specific tr
20	49	45.8	367	2 S59329	T-cell-specific tr
21	48	44.9	269	2 B38095	T-cell-specific tr
22	48	44.9	272	2 A38900	T-cell-specific tr
23	48	44.9	303	2 JH0401	hypothetical protein
24	48	44.9	351	2 T23851	probable polynucle
25	48	44.9	453	2 D81870	polyA polymerase N
26	48	44.9	453	2 H81151	probable ATP-depen
27	48	44.9	454	2 E64816	probable ATP-depen
28	48	44.9	455	2 D85588	probable ATP-depen
29	48	44.9	455	2 C90738	probable ATP-depen

ALIGNMENTS

RESULT 1

T09384 trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate HIV-1)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Accession: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 31-Dec-2004

R:Michael, N.L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.; Birx, J.; Virol., 69, 4228-4236, 1995

A:Title: Defective accessory genes in a human immunodeficiency virus type 1-infected long-term culture

A:Reference number: 216654; PMID: 95267475; PMID: 7763682

A:Accession: T09384

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-71 <MIC>

A:Cross-references: UNIPARC:UPI0000FF00C; EMBL:U24451; NID:9829440; PID: 2990041

A:Gene: tat

C:Superfamily: leukemia virus trans-activating transcription regulator

C:Keywords: transcription

Query Match Score 71.0%; Best Local Similarity 65.0%; Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YGRKKRRRKRKPKASADGHR 20

Db 47 YGRKKRRRKRSPQDSEAHQ 66

RESULT 2

A25700 trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate HIV-1)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Accession: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 31-Dec-2004

R:Sodroski, J.; Patarca, R.; Rosen, C.; Wong-Staal, F.; Haseltine, W.

A:Reference number: A25700

A:Accession: A25700

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-86 <SOd>

A:Cross-references: UNIPARC:P04610; UNIPARC:UPI0000111F40

C:Superfamily: leukemia virus trans-activating transcription regulator

Query Match Score 66.4%; Best Local Similarity 65.0%; Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRRRKRKPKASADGHR 20

Db 47 YGRKKRRRKRSPQGSQHQ 66

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-2004
 C;Accession: E44001
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Title: Complete nucleotide sequence, genome organization, and biological properties of
 C;Reference number: A44001; MUID:93021387; PMID:1404605
 A;Accession: E44001
 A;Molecule type: DNA
 A;Residues: 1-101 <ALI>
 A;Cross-references: UNIPARC:P35965; UNIPARC:UPI0000136937; GB:M93258
 A;Gene: tat
 A;Introns: 72/2
 C;Superfamily: AIDS; immunodeficiency; transcription regulator
 C;Keywords: AIDS, immunodeficiency; transcription regulation

Query Match 66.4%; Score 71; DB 1; Length 101;
 Best Local Similarity 65.0%; Pred. No. 0.0086;
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRQRKPKASADGHR 20
 Db 47 YGRKKRQRKPKASADGHR 20

RESULT 6
 T09446
 tat protein - human immunodeficiency virus type 1 (strain JRF1)
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Accession: T09446
 R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,
 submitted to the EMBL Data Library, July 1996
 A;Reference number: Z16673
 A;Accession: T09446
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-101 <PAN>
 A;Cross-references: UNIPROT:Q75758; UNIPARC:UPI0000109776; EMBL:U63632; NID:91465777; PII
 C;Genetics:
 C;Keywords: AIDS; immunodeficiency

Query Match 66.4%; Score 71; DB 2; Length 101;
 Best Local Similarity 65.0%; Pred. No. 0.0086;
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRQRKPKASADGHR 20
 Db 47 YGRKKRQRKPKASADGHR 20

RESULT 7
 T01665
 tat protein - human immunodeficiency virus type 1
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Accession: T01665
 R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
 Cell 46, 63-74, 1986
 A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isolates
 A;Reference number: Z14389; MUID:86245056; PMID:2424612
 A;Accession: T01665
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-87 <ALI>
 A;Cross-references: UNIPROT:P04613; UNIPARC:UPI00001132A9; EMBL:K03456; NID:960228; PIDN
 C;Genetics:
 C;Keywords: AIDS; immunodeficiency

Query Match 65.4%; Score 70; DB 2; Length 87;

RESULT 5
 E44001
 trans-activating transcription regulator - human immunodeficiency virus type 1 (strain Y
 N;Alternative names: tat protein
 C;Species: human immunodeficiency virus type 1, HIV-1
 A;Note: host Homo sapiens (man)

Best Local Similarity 65.0%; Pred. No. 0.01; Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YGRKRRQRKRKPASADGHR 20
Db 47 YGRKRRQRKRPPQGNQAHQ 66

RESULT 8

TNfJND trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Dec-2004 C;Accession: JQ0071 R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.; Gene 81; 275-284; 1986 A;Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunodeficiency virus. J. Virol. 61: 275-284. PMID:2806917 A;Reference number: JQ0065; MUID:190034200; PMID:2806917 A;Accession: JQ0071 A;Molecule type: DNA A;Residues: 1-86 <SPI> A;Cross-references: UNIPROT:P18804; UNIPARC:UPI000011DSD6; GB:M27323; PIDN: JQ591

C;Genetics:
C;Superfamily: AIDS; immunodeficiency; transcription regulator

Query Match 62.6%; Score 67; DB 1; Length 86;
Best Local Similarity 60.0%; Pred. No. 0.036; Mismatches 2; Indels 6; Gaps 0;

Qy 1 YGRKRRQRKRKPASADGHR 20
Db 47 YGRKRRQRKRKPQGDQAHQ 66

RESULT 9

TNfJH4 trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004 C;Accession: B25523 R;Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, Proc. Natl. Acad. Sci. U.S.A. 83: 8380-8384, 1986 A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human immunodeficiency virus. J. Virol. 61: 8380-8384. PMID:3490666 A;Accession: B25523 A;Molecule type: DNA A;Residues: 1-72 <DEB> A;Cross-references: UNIPARC:UPI0000174A55; GB:M13137; PID:9326460 A;Note: the GenBank entry ADRE3AA PID:920908 differs from the published sequence in trans-activating transcription regulator

C;Genetics:
C;Superfamily: AIDS; immunodeficiency virus type 1, HIV-1 A;Gene: tat C;Keywords: transcription regulation

Query Match 59.8%; Score 64; DB 1; Length 72;
Best Local Similarity 60.0%; Pred. No. 0.057; Mismatches 2; Indels 6; Gaps 0;

Qy 1 YGRKRRQRKRKPASADGHR 20
Db 47 YGRKRRQRRAHQDSQNHQ 66

RESULT 10

TNfJZR trans-activating transcription regulator - human immunodeficiency virus Zr-6 C;Species: human immunodeficiency virus Zr-6 A;Accession: C26192 C;Title: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 31-Dec-2004 R;srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu

Gene 52, 71-82, 1987
A;Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotide sequence and comparison with other human immunodeficiency viruses
A;Reference number: A26192; MUID:87248099; PMID:3036660

A;Accession: C26192
A;Molecule type: DNA
A;Residues: 1-86 <SR1>
A;Cross-references: UNIPROT:P04609; UNIPARC:UPI000013693A; GB:K03458; PID:93248099

C;Genetics:
A;Gene: tat

A;Introns: 72/3
C;Superfamily: leukemia virus trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 57.9%; Score 62; DB 1; Length 86;
Best Local Similarity 60.0%; Pred. No. 0.12; Mismatches 12; Conservative 1; Indels 0; Gaps 0;

Qy 1 YGRKRRQRKRKPASADGHR 20
Db 47 YGRKRRQRKRPSQGGTHQ 66

RESULT 11

JC591

transactivator protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 31-Dec-2004
C;Accession: JC591
R;Hoffmann, S.; Willbold, D.
Blochem. Biophys. Res. Commun. 235, 806-811, 1997
A;Title: A selection system to study protein-DNA interactions: Functional display of HIV
A;Reference number: JC5591; MUID:9750867; PMID:9207243

A;Molecule type: protein
A;Residues: 1-86 <HO2>
A;Cross-references: UNIPARC:UPI000017865E

C;Comment: This protein is a key regulatory protein in the viral replication cycle and belongs to the EMBL Data Library, July 1989
C;Superfamily: leukemia virus trans-activating transcription regulator

F:22-31/Region: cysteine-rich

Query Match 57.9%; Score 62; DB 2; Length 86;
Best Local Similarity 60.0%; Pred. No. 0.12; Mismatches 12; Conservative 1; Indels 0; Gaps 0;

Qy 1 YGRKRRQRKRKPASADGHR 20
Db 47 YGRKRRQRKRPSQGGTHQ 66

RESULT 12

SS5381

trans-activating transcription regulator - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 31-Dec-2004
C;Accession: SS54381
R;Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A;Reference number: SS54377

A;Accession: SS4381
A;Status: Preliminary
A;Molecule type: genomic RNA
A;Residues: 1-86 <THE>
A;Cross-references: UNIPROT:P12506; UNIPARC:UPI0000136938; EMBL:M22639; PID:9329377; PID:9329378

C;Genetics:
A;Introns: 72/2
C;Superfamily: leukemia virus trans-activating transcription regulator

Query Match 57.9%; Score 62; DB 2; Length 86;
Best Local Similarity 60.0%; Pred. No. 0.12; Mismatches 7; Indels 0; Gaps 0;

Qy 1 YGRKRRQRKRKPASADGHR 20

A; Status: preliminary; not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 1-399 <WAT>
 A; Cross-references: UNIPROT:Q9UUT2; UNIPARC:UPI0000052242
 C; Keywords: T-cell receptor
 F; 296-371/Domain: HMG box homology <HMG1>

RESULT 13
 B70681 probable rne protein - Mycobacterium tuberculosis (strain H37RV)
 C; Species: Mycobacterium tuberculosis
 C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C; Accession: B70681
 R; Cole, S.T.; Broscb, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
 R; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 R; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 R; Nature 393, 53-54, 1998
 A; Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A; Reference number: A70500; PMID:8295987;
 A; Accession: B70681
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-953 <COL>
 A; Cross-references: UNIPROT:P71905; UNIPARC:UPI000005011; GB:281451; GB:AL123456; NID:9
 C; Genetics:
 A; Gene: rne

Query Match 49.5%; Score 53; DB 2; Length 953;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 RKKRQRKRKPASAD 17
 Db 230 RRRRRRRRSAGD 244

RESULT 14
 B39625 T-cell receptor alpha enhancer-binding protein, short form - human
 C; Species: Homo sapiens (man)
 C; Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 31-Dec-2004
 C; Accession: B39625
 R; Waterman, M.L.; Fischer, W.H.; Jones, K.A.
 Genes Dev. 5, 656-669, 1991
 A; Title: A thymus-specific member of the HMG protein family regulates the human T cell
 A; Reference number: A39625; PMID:9118420; PMID:201090
 A; Accession: B39625
 A; Status: preliminary; not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 1-371 <WAT>
 A; Cross-references: UNIPARC:UPI000017A223
 C; Keywords: T-cell receptor
 F; 268-343/Domain: HMG box homology <HMG1>

Query Match 46.7%; Score 50; DB 2; Length 371;
 Best Local Similarity 50.0%; Pred. No. 16;
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 YGRKRRQRKRKPASADG 18
 Db 344 YGKRRQRKRKPASAG 361

RESULT 15
 A39625 T-cell receptor alpha enhancer-binding protein, long form - human
 C; Species: Homo sapiens (man)
 C; Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 31-Dec-2004
 C; Accession: A39625
 R; Waterman, M.L.; Fischer, W.H.; Jones, K.A.
 Genes Dev. 5, 656-669, 1991
 A; Title: A thymus-specific member of the HMG protein family regulates the human T cell
 A; Reference number: A39625; PMID:9118420; PMID:201090
 A; Accession: A39625

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OM protein - protein search, using sw mode!

Run on: August 24, 2006, 23:39:22 ; Search time 32 Seconds
(without alignments)

42.764 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 107

Sequence: 1 YGRKRRQRRKPASADGHR 20

Scoring table: BLOSUM62

Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New:^{*}

1: /EMC_Celerra_SIDS/ptodata/1/pubpaas/us09_NEW_PUB.PEP:
2: /EMC_Celerra_SIDS/ptodata/1/pubpaas/us06_NEW_PUB.PEP:
3: /EMC_Celerra_SIDS/ptodata/1/pubpaas/us07_NEW_PUB.PEP:
4: /EMC_Celerra_SIDS/ptodata/1/pubpaas/us08_NEW_PUB.PEP:
5: /EMC_Celerra_SIDS/ptodata/1/pubpaas/oct_NEW_PUB.PEP:
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7: /EMC_Celerra_SIDS/ptodata/1/pubpaas/us11_NEW_PUB.PEP:
8: /EMC_Celerra_SIDS/ptodata/1/pubpaas/us60_NEW_PUB.PEP:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-10-539-677-37

; Sequence 37, Application US/10539677
; Publication No. US200601049881
; GENERAL INFORMATION:
; APPLICANT: University of Maryland Biotechnology Institute
; PAUZA, C. David
; ATTORNEY: Tikhonov, Ilia
; TITLE OF INVENTION: VACCINES AGAINST HIV-1 PROTEIN TO GENERATE NEUTRALIZING ANTIBODIES
; FILE REFERENCE: 4115-194
; CURRENT APPLICATION NUMBER: US/10/539,677
; CURRENT FILING DATE: 2005-06-16
; PRIOR APPLICATION NUMBER: US 60/434,368
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct

US-10-539-677-37

Query Match 66.4%; Score 71; DB 6; Length 20;
Best Local Similarity 68.4%; Pred. No. 0.002; Indels 0; Gaps 0;

Matches 13; Conservative 2; Mismatches 4;

Qy 1 YGRKRRQRRKPASADGH 19
Db 2 YGRKRRQRRKPASSEDH 20

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	66.4	20	US-10-539-677-37	Sequence 37, App1
2	71	66.4	36	7 US-11-285-920-6	Sequence 6, App1
3	71	66.4	229	6 US-10-533-841-54	Sequence 5, App1
4	71	66.4	293	6 US-10-533-841-52	Sequence 52, App1
5	71	66.4	715	6 US-10-533-841-60	Sequence 60, App1
6	71	66.4	779	6 US-10-533-841-58	Sequence 58, App1
7	71	66.4	1078	6 US-10-533-841-77	Sequence 67, App1
8	71	66.4	1141	6 US-10-533-841-71	Sequence 71, App1
9	71	66.4	1141	6 US-10-533-841-79	Sequence 79, App1
10	71	66.4	1141	6 US-10-533-841-81	Sequence 81, App1
11	71	66.4	1141	6 US-10-533-841-83	Sequence 83, App1
12	71	66.4	1142	6 US-10-533-841-69	Sequence 69, App1
13	71	66.4	1142	6 US-10-533-841-73	Sequence 73, App1
14	71	66.4	1142	6 US-10-533-841-75	Sequence 75, App1
15	71	66.4	1142	6 US-10-533-841-77	Sequence 77, App1
16	70	65.4	20	6 US-10-539-677-36	Sequence 36, App1
17	70	65.4	29	7 US-11-251-734-4	Sequence 4, App1
18	65	60.7	20	6 US-10-539-677-38	Sequence 36, App1
19	64	59.8	14	7 US-11-142-051-4	Sequence 4, App1
20	62	57.9	20	6 US-10-539-677-34	Sequence 34, App1
21	62	57.9	34	7 US-11-223-610-46	Sequence 46, App1
22	61	57.0	20	6 US-10-539-677-35	Sequence 35, App1
23	58	54.2	11	6 US-10-547-530-78	Sequence 78, App1
24	58	54.2	11	6 US-10-518-710-4	Sequence 4, App1
25	58	54.2	11	6 US-10-559-806A-1	Sequence 1, App1

RESULT 2
US-11-286-920-6

; Sequence 6, Application US/11286920
; Publication No. US2006016688A1
; GENERAL INFORMATION:
; APPLICANT: Washington University
; HOCHKISS, Richard
; ATTORNEY: Piwnica-Worms, David
; TITLE OF INVENTION: Membrane-Permeant Peptide Complexes for Treatment of Sepsis
; FILE REFERENCE: 60005161-0204
; CURRENT APPLICATION NUMBER: US/11/286,920
; CURRENT FILING DATE: 2005-11-23
; PRIOR APPLICATION NUMBER: US 10/374,035

```

; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 52
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 Nef-Tatm fusion
US-10-533-841-52

Query Match 66.4%; Score 71; DB 6; Length 293;
Best Local Similarity 65.0%; Pred. No. 0.023; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKRRQRKRKPASADGHR 20
Db 254 YGRKRRQRKRKPQGSQTHQ 273

RESULT 5
US-10-533-841-60
; Sequence 60, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 60
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 ds-SP120C Nef-Tatm fusion
US-10-533-841-60

Query Match 66.4%; Score 71; DB 6; Length 715;
Best Local Similarity 65.0%; Pred. No. 0.05; Mismatches 2; Indels 5; Gaps 0;

Qy 1 YGRKRRQRKRKPASADGHR 20
Db 676 YGRKRRQRKRKPQGSQTHQ 695

RESULT 6
US-10-533-841-58
; Sequence 58, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 58
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 tNef-Tatm fusion
US-10-533-841-54

Query Match 66.4%; Score 71; DB 6; Length 229;
Best Local Similarity 65.0%; Pred. No. 0.018; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKRRQRKRKPASADGHR 20
Db 190 YGRKRRQRKRKPQGSQTHQ 209

RESULT 4
US-10-533-841-52
; Sequence 52, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```

OTHER INFORMATION: HIV-1 ds-gp120c' US-10-533-841-58

Query Match	66.4%	Score 71;	DB 6;	Length 779;
Best Local Similarity	65.0%	Pred. No.	0.054;	
Matches 13;	Conservative 2;	Mismatches 5;	Indels	

Qy 1 YGRKKRRRKRKPASADGHR 20
Db 740 YGRKKRRRKRPPQGSQTHQ 759

RESULT 7
US-10-533-841-67
Sequence 67, Application US/10533841
Publication No. US20060142221A1
GENERAL INFORMATION:
APPLICANT: ERTL, Peter F.
TITLE OF INVENTION: Vaccine
FILE REFERENCE: PG023
CURRENT APPLICATION NUMBER: US/10/533,841
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: PCT/EP 03/12402
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: GB 0225788.9
PRIOR FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 67
LENGTH: 1078
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV-1 ds-gp120c p17/24 trNEF Tatm fusion

US-10-533-841-67

Query Match	66.4%	Score 71;	DB 6;	Length 1078;
Best Local Similarity	65.0%	Pred. No.	0.073;	
Matches 13;	Conservative 2;	Mismatches 5;	Indels	

Qy 1 YGRKKRRRKRKPASADGHR 20
Db 1039 YGRKKRRRKRPPQGSQTHQ 1058

RESULT 8
US-10-533-841-71
Sequence 71, Application US/10533841
Publication No. US20060142221A1
GENERAL INFORMATION:
APPLICANT: ERTL, Peter F.
TITLE OF INVENTION: Vaccine
FILE REFERENCE: PG023
CURRENT APPLICATION NUMBER: US/10/533,841
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: PCT/EP 03/12402
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: GB 0225788.9
PRIOR FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 71
LENGTH: 1141
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV-1 ds-gp120c p17/24 mNEF Tatm fusion

US-10-533-841-71

Query Match	66.4%	Score 71;	DB 6;	Length 1141;
Best Local Similarity	65.0%	Pred. No.	0.077;	
Matches 13;	Conservative 2;	Mismatches 5;	Indels	

```

RESULT 9
US-10-533-841-79
; Sequence 79, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
;   APPLICANT: ERTL, Peter F.
;   TITLE OF INVENTION: Vaccine
;   FILE REFERENCE: PG5023
;   CURRENT APPLICATION NUMBER: US/10/53
;   CURRENT FILING DATE: 2005-05-04
;   PRIOR APPLICATION NUMBER: PCT/EP 03/
;   PRIOR FILING DATE: 2003-03-11
;   PRIOR APPLICATION NUMBER: GB 0225788
;   PRIOR FILING DATE: 2002-11-05
;   NUMBER OF SEQ ID NOS: 89
;   SOFTWARE: FastSEQ For Windows Version
;   SEQ ID NO 79
;   LENGTH: 1141
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HIV-1 ds-gp120C
US-10-533-841-79

Query Match       66.4%; Score
Best Local Similarity 65.0%; Pred.
Matches 13; Conservative 2; Mi

Qy      1 YGRKRRQRKRKPASADGHR 20
Db      1 YGRKRRQRKRKPASADGHR 20
Db      1102 YGRKRRQRKRPPQSQTHQ 1121

RESULT 10
US-10-533-841-81
; Sequence 81, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
;   APPLICANT: ERTL, Peter F.
;   TITLE OF INVENTION: Vaccine
;   FILE REFERENCE: PG5023
;   CURRENT APPLICATION NUMBER: US/10/53
;   CURRENT FILING DATE: 2005-05-04
;   PRIOR APPLICATION NUMBER: PCT/EP 03/
;   PRIOR FILING DATE: 2003-03-11
;   PRIOR APPLICATION NUMBER: GB 0225788
;   PRIOR FILING DATE: 2002-11-05
;   NUMBER OF SEQ ID NOS: 89
;   SOFTWARE: FastSEQ For Windows Version
;   SEQ ID NO 81
;   LENGTH: 1141
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HIV-1 ds-gp120C
US-10-533-841-81

Query Match       66.4%; Score
Best Local Similarity 65.0%; Pred.
Matches 13; Conservative 2; Mi

Qy      1 YGRKRRQRKRKPASADGHR 20
Db      1 YGRKRRQRKRKPASADGHR 20
Db      1102 YGRKRRQRKRPPQSQTHQ 1121

RESULT 11
US-10-533-841-83

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; Sequence 83, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIORITY NUMBER: PCT/EP 03/12402
; PRIORITY FILING DATE: 2003-03-11
; PRIORITY APPLICATION NUMBER: GB 0225788.9
; PRIORITY FILING DATE: 2002-11-05
; PRIORITY NUMBER: SEQ ID NOS: 89
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 83
; LENGTH: 1141
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 ds-gp120c p17/24 L1-NeF Tatm fusion
US-10-533-841-83

Query Match          66.4%;  Score 71;  DB 6;  Length 1141;
Best Local Similarity 65.0%;  Pred. No. 0.077;  Mismatches 5;  Indels 0;  Gaps 0;
Matches 13;  Conservative 2;  Mismatches 5;  Indels 0;  Gaps 0;

RESULT 12
US-10-533-841-69
; Sequence 69, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIORITY NUMBER: PCT/EP 03/12402
; PRIORITY FILING DATE: 2003-03-11
; PRIORITY APPLICATION NUMBER: GB 0225788.9
; PRIORITY FILING DATE: 2002-11-05
; PRIORITY NUMBER: SEQ ID NOS: 89
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 69
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 ds-gp120c p17/24 NeF Tatm fusion
US-10-533-841-69

Query Match          66.4%;  Score 71;  DB 6;  Length 1142;
Best Local Similarity 65.0%;  Pred. No. 0.077;  Mismatches 5;  Indels 0;  Gaps 0;
Matches 13;  Conservative 2;  Mismatches 5;  Indels 0;  Gaps 0;

RESULT 13
US-10-533-841-73
; Sequence 73, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIORITY APPLICATION NUMBER: PCT/EP 03/12402
; PRIORITY FILING DATE: 2003-03-11
; PRIORITY APPLICATION NUMBER: GB 0225788.9
; PRIORITY FILING DATE: 2002-11-05
; PRIORITY NUMBER: SEQ ID NOS: 89
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0

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; SEQ ID NO: 77
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 ds-gp120c p17/24 Ll-Nef Tarm fusion
US-10-533-81-77

Query Match          66.4%; Score 71; DB 6; Length 1142;
Best Local Similarity 65.0%; Prod. No. 0.077;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      1 YGRKKRKRRRKPAASADGHR 20
       ||||| | | | | | | ; | ;
Db      1103 YGRKKRKRRRKPAASADGHRQ 1122

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Search completed: August 24, 2006, 23:42:57
Job time: 33 SECs

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OM protein - protein search, using sw model.

Run on: August 24, 2006, 23:38:27 ; Search time 185 Seconds (without alignments)

50.079 Million cell updates/sec

Title: US-10-814-109-2

Pearl score: 107

Sequence: 1 YGRKCKRQRRRKPAASADGHR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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6: /EMC_Celerra_SIDS3_ptoodata/2/pubpaas/US11_PUBCOMB.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	100.0	20	5 US-10-814-109-2	Sequence 2, Appli
2	79	73.8	101	4 US-10-190-435-211	Sequence 211, Appli
3	78	72.9	101	4 US-10-190-435-220	Sequence 212, Appli
4	78	72.9	101	5 US-10-780-507-110	Sequence 213, Appli
5	75	70.1	101	4 US-10-190-435-227	Sequence 214, Appli
6	75	70.1	101	6 US-11-205-883A-6	Sequence 215, Appli
7	75	70.1	1896	4 US-10-296-734-393	Sequence 216, Appli
8	75	70.1	5747	4 US-10-296-734-405	Sequence 217, Appli
9	74	69.2	101	4 US-10-190-435-213	Sequence 218, Appli
10	74	69.2	101	5 US-10-501-223-1	Sequence 219, Appli
11	74	69.2	101	5 US-10-501-223-20	Sequence 220, Appli
12	74	69.2	101	5 US-10-501-223-41	Sequence 221, Appli
13	74	69.2	101	5 US-10-501-223-42	Sequence 222, Appli
14	74	69.2	101	5 US-10-501-223-41	Sequence 223, Appli
15	74	69.2	101	5 US-10-501-223-42	Sequence 224, Appli
16	74	69.2	101	5 US-10-501-223-43	Sequence 225, Appli
17	74	69.2	101	5 US-10-501-223-74	Sequence 226, Appli
18	73	68.2	101	6 US-11-135-597-219	Sequence 227, Appli
19	73	68.2	102	4 US-10-770-668-50	Sequence 228, Appli
20	73	68.2	1893	4 US-10-296-734-399	Sequence 229, Appli
21	72	67.3	99	4 US-10-190-435-215	Sequence 230, Appli
22	72	67.3	99	4 US-10-190-435-218	Sequence 231, Appli
23	72	67.3	100	5 US-10-969-191-16	Sequence 232, Appli
24	72	67.3	101	4 US-10-190-435-208	Sequence 233, Appli
25	72	67.3	101	4 US-10-190-435-210	Sequence 234, Appli
26	72	67.3	101	4 US-10-190-435-212	Sequence 235, Appli
27	72	67.3	101	4 US-10-190-435-216	Sequence 236, Appli

ALIGNMENTS

RESULT 1
US-10-814-109-2

; Sequence 2, Application US/10814109
; Publication No. US2005022042A1

; GENERAL INFORMATION:
; APPLICANT: Salter, Michael
; INVENTOR: Gingrich, Jeffrey
; TITLE OF INVENTION: Method For Modification of NMDA Receptors Through Inhibition of S, T, and C Receptors
; FILE REFERENCE: 2560_004
; CURRENT APPLICATION NUMBER: US/10/814_109
; CURRENT FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-814-109-2

Query Match 100.0%; Score 107; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5e-03; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKCKRQRRRKPAASADGHR 20
Db 1 YGRKCKRQRRRKPAASADGHR 20

RESULT 2
US-10-190-435-211

; Sequence 211, Application US/10190435
; Publication No. US20030143248A1

; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan W.
; INVENTOR: BARNETT, Susan W.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP/8133.003 / 2303-18133
; CURRENT APPLICATION NUMBER: US/10/190_435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 211

; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Tat TV006
 US-10-190-435-211

Query Match Score 79; DB 4; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0019; Indels 0; Gaps 0;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRKPASADGHR 20
 Db 47 YGRKKRQRRSTPPSEGHQ 66

RESULT 3
 US-10-190-435-221
 Sequence 221, Application US/10190435
 Publication No. US20030143248A1

GENERAL INFORMATION:
 APPLICANT: ZUR MEGEDE, Jan
 APPLICANT: BARNETT, Susan W.
 APPLICANT: LIAN, Ying
 APPLICANT: ENGELBRECHT, Susan
 APPLICANT: VAN RENSBURG, Estrelita J.

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
 TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
 FILE REFERENCE: PP1813.003 / 2302-18133

CURRENT APPLICATION NUMBER: US10/190,435
 CURRENT FILING DATE: 2002-12-30
 NUMBER OF SEQ ID NOS: 319
 SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 221
 LENGTH: 101
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Tat 301904-Ind
 US-10-190-435-221

Query Match Score 79; DB 4; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0026; Indels 0; Gaps 0;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRKPASADGHR 20
 Db 47 YGRKKRQRRAPQSSDHQ 66

RESULT 4
 US-10-780-507-110
 Sequence 110, Application US/10780507
 Publication No. US20050137387A1

GENERAL INFORMATION:
 APPLICANT: MULLINS, James I.
 APPLICANT: RODRIGO, Allen G.
 APPLICANT: LEARN, Gerald H.
 APPLICANT: LI, Fusheng
 APPLICANT: NICKLE, David C.
 APPLICANT: JENSEN, Mark A.

TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPOUNDS
 FILE REFERENCE: 16336-00120US
 CURRENT APPLICATION NUMBER: US/10/780,507
 CURRENT FILING DATE: 2004-02-17
 PRIOR APPLICATION NUMBER: US 10/204,204
 PRIOR FILING DATE: 2001-02-16
 PRIOR APPLICATION NUMBER: PCT/US01/05288
 PRIOR FILING DATE: 2001-02-16
 PRIOR APPLICATION NUMBER: US 60/183,659
 PRIOR FILING DATE: 2000-02-18
 PRIOR APPLICATION NUMBER: US 60/447,586
 PRIOR FILING DATE: 2003-02-14
 NUMBER OF SEQ ID NOS: 125
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 110
 LENGTH: 101

; TYPE: PRT ; Artificial sequence
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Most recent common ancestor reconstructions of clade C tat protein
 ; OTHER INFORMATION: n sequence
 US-10-780-507-110

Query Match Score 78; DB 5; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0026; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRKPASADGHR 20
 Db 47 YGRKKRQRRAPQSSDHQ 66

RESULT 5
 US-10-190-435-227
 Sequence 227, Application US/10190435
 Publication No. US20030143248A1

GENERAL INFORMATION:
 APPLICANT: ZUR MEGEDE, Jan
 APPLICANT: BARNETT, Susan W.
 APPLICANT: LIAN, Ying
 APPLICANT: ENGELBRECHT, Susan
 APPLICANT: VAN RENSBURG, Estrelita J.

TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
 TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
 FILE REFERENCE: PP1813.003 / 2302-18133
 CURRENT APPLICATION NUMBER: US/10/190,435
 CURRENT FILING DATE: 2002-12-30
 NUMBER OF SEQ ID NOS: 319
 SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 227
 LENGTH: 101
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Tat C2220-Bth
 ; TYPE: PRT ; Artificial Sequence
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Tat C2220-Bth
 ; NAME/KEY: SITE
 ; LOCATION: (40)
 ; OTHER INFORMATION: where Xaa = unknown amino acid

US-10-190-435-227

Query Match Score 75; DB 4; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.007; Indels 4; Gaps 0;

Qy 1 YGRKKRQRRKPASADGHR 20
 Db 47 YGRKKRQRRAPQSSDHQ 66

RESULT 6
 US-11-205-883A-6
 Sequence 6, Application US/11205883A

GENERAL INFORMATION:
 APPLICANT: PAYNE, SHELLIE M.
 APPLICANT: DUDLEY, JAQUELINE P.
 APPLICANT: SELIGER, STEFAN S.
 APPLICANT: FENG, ZHENGYU

TITLE OF INVENTION: BACTERIAL VECTOR SYSTEMS
 FILE REFERENCE: CLPR-030US
 CURRENT APPLICATION NUMBER: US/11/205,883A
 CURRENT FILING DATE: 2005-08-17
 PRIOR APPLICATION NUMBER: 60/1602,276
 PRIOR FILING DATE: 2004-08-17
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 6
 LENGTH: 101

TYPE: PRT ; ORGANISM: Artificial Sequence ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic ; OTHER INFORMATION: Peptide US-11-205-8B3A-6

Query Match 70.1%; Score 75; DB 6; Length 101; Best Local Similarity 70.0%; Pred. No. 0.007; Indels 4; Gaps 0; Matches 14; Conservative 2; Mismatches 4; Indexes 0; Gaps 0;

Qy 1 YGRKERRQRRKPASADGHR 20
Db 47 YGRKERRQRRKPASADGHR 66

RESULT 7
US-10-296-734-393
; Sequence 393, Application US/10296734
; Publication No. US20040054137A1.
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ranshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 393
; LENGTH: 1896

TYPE: PRT ; ORGANISM: Artificial ; FEATURE: OTHER INFORMATION: HIV cassette A1

Query Match 70.1%; Score 75; DB 4; Length 1896; Best Local Similarity 70.0%; Pred. No. 0.11; Indels 4; Gaps 0; Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRKPASADGHR 20
Db 186 YGRKERRQRRKPASADGHR 205

RESULT 8
US-10-296-734-405
; Sequence 405, Application US/10296734
; Publication No. US20040054137A1.
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ranshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 405
; LENGTH: 5747

TYPE: PRT ; ORGANISM: Artificial ; OTHER INFORMATION: HIV complete bovine US-10-296-734-405

Query Match 70.1%; Score 75; DB 4; Length 5747; Best Local Similarity 70.0%; Pred. No. 0.31;

Matches 14; Conservative 2; Mismatches 4; Indexes 0; Gaps 0;

Qy 1 YGRKERRQRRKPASADGHR 20
Db 47 YGRKERRQRRKPASADGHR 66

RESULT 9
US-10-190-435-213
; Sequence 213, Application US/10190435
; Publication No. US2003014348A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGIDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PPI8133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 213
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tat TV008
US-10-190-435-213

Query Match 69.2%; Score 74; DB 4; Length 101; Best Local Similarity 65.0%; Pred. No. 0.0096; Mismatches 3; Indexes 0; Gaps 0;

Qy 1 YGRKERRQRRKPASADGHR 20
Db 47 YGRKERRQRRKPASADGHR 66

RESULT 10
US-10-301-223-1
; Sequence 1, Application US/10501223
; Publication No. US2005016416A1
; GENERAL INFORMATION:
; APPLICANT: GUILLON, CHRISTOPHE
; APPLICANT: CHEDAL-BORNU, AURELIE
; APPLICANT: VERRIER, BERNARD
; TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS
; FILE REFERENCE: 0508-1107
; CURRENT APPLICATION NUMBER: US/10/501,223
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: PCT/FR03/00051
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: FR 02/00319
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 1
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-301-223-1

Query Match 69.2%; Score 74; DB 5; Length 101; Best Local Similarity 65.0%; Pred. No. 0.0096; Mismatches 3; Indexes 0; Gaps 0;

Qy 1 YGRKERRQRRKPASADGHR 20
Db 47 YGRKERRQRRKPASADGHR 66

RESULT 11
US-10-501-223-20
Sequence 20, Application US/10501223
; Publication No. US20050164164A1
GENERAL INFORMATION:
; APPLICANT: GUILLOIN, CHRISTOPHE
; APPLICANT: CHEDAL-BORNU, AURELIE
; APPLICANT: GUILLON, CHRISTOPHE
; APPLICANT: CHEDAL-BORNU, AURELIE
; APPLICANT: VERRIER, BERNARD
; APPLICANT: MANDRAND, BERNARD
TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS
FILE REFERENCE: 0508-1107
CURRENT APPLICATION NUMBER: US/10/501,223
CURRENT FILING DATE: 2004-07-12
PRIORITY NUMBER: PCT/FR03/00051
PRIOR FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: FR 02/00319
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 141
SOFTWARE: PatentIn version 3.3
SEQ ID NO 20
LENGTH: 101
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G79A-K89L
; OTHER INFORMATION: Mutant of Tat protein
US-10-501-223-20

Query Match 69.2%; Score 74; DB 5; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.0096;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRKPASADGHR 20
Db 47 YGRKERRQRRKPASADGHR 66

RESULT 12
US-10-501-223-21
Sequence 21, Application US/10501223
; Publication No. US20050164164A1
GENERAL INFORMATION:
; APPLICANT: GUILLOIN, CHRISTOPHE
; APPLICANT: CHEDAL-BORNU, AURELIE
; APPLICANT: VERRIER, BERNARD
; APPLICANT: MANDRAND, BERNARD
TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS
FILE REFERENCE: 0508-1107
CURRENT APPLICATION NUMBER: US/10/501,223
CURRENT FILING DATE: 2004-07-12
PRIORITY NUMBER: PCT/FR03/00051
PRIOR FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: FR 02/00319
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 141
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21
LENGTH: 101
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G79A-E92Q
; OTHER INFORMATION: Mutant of Tat protein
US-10-501-223-21

Query Match 69.2%; Score 74; DB 5; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.0096;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRKPASADGHR 20

RESULT 13
US-10-501-223-22
Sequence 22, Application US/10501223
; Publication No. US20050164164A1
GENERAL INFORMATION:
; APPLICANT: GUILLON, CHRISTOPHE
; APPLICANT: CHEDAL-BORNU, AURELIE
; APPLICANT: VERRIER, BERNARD
; APPLICANT: MANDRAND, BERNARD
TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS
FILE REFERENCE: 0508-1107
CURRENT APPLICATION NUMBER: US/10/501,223
CURRENT FILING DATE: 2004-07-12
PRIORITY NUMBER: PCT/FR03/00051
PRIOR FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: FR 02/00319
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 141
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22
LENGTH: 101
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: K89L-E92Q
; OTHER INFORMATION: Mutant of Tat protein
US-10-501-223-22

Query Match 69.2%; Score 74; DB 5; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.0096;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRKPASADGHR 20

RESULT 14
US-10-501-223-41
Sequence 41, Application US/10501223
; Publication No. US20050164164A1
GENERAL INFORMATION:
; APPLICANT: GUILLON, CHRISTOPHE
; APPLICANT: CHEDAL-BORNU, AURELIE
; APPLICANT: VERRIER, BERNARD
; APPLICANT: MANDRAND, BERNARD
TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS
FILE REFERENCE: 0508-1107
CURRENT APPLICATION NUMBER: US/10/501,223
CURRENT FILING DATE: 2004-07-12
PRIORITY NUMBER: PCT/FR03/00051
PRIOR FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: FR 02/00319
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 141
SOFTWARE: PatentIn version 3.3
SEQ ID NO 41
LENGTH: 101
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C27S-G79A-K89L
; OTHER INFORMATION: Mutant of Tat protein
US-10-501-223-41

Query Match 69.2%; Score 74; DB 5; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.0096;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRKPASADGHR 20

Db 47 |||||::|||: YGRKRRQRRSPQDSETHQ 66

RESULT 15
 US-10-501-223-42
 ; Sequence 42, Application US/10501223
 ; Publication No. US2005016164AA
 ; GENERAL INFORMATION:
 ; APPLICANT: GUILLOU, CHRISTOPHE
 ; APPLICANT: CHEDAL-BORNU, AURELIE
 ; APPLICANT: VERRIER, BERNARD
 ; APPLICANT: MANDRAND, BERNARD
 ; TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS
 ; FILE REFERENCE: 0508-1107
 ; CURRENT APPLICATION NUMBER: US/10/501,223
 ; CURRENT FILING DATE: 2004-07-12
 ; PRIOR APPLICATION NUMBER: PCT/FR03/00051
 ; PRIOR FILING DATE: 2003-01-09
 ; PRIOR APPLICATION NUMBER: FR 02/00319
 ; PRIOR FILING DATE: 2002-01-11
 ; NUMBER OF SEQ ID NO: 141
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 42
 ; LENGTH: 101
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: C27S-G79A-E92Q
 ; OTHER INFORMATION: mutant of Tat protein
 US-10-501-223-42

Query Match 69.2%; Score 74; DB 5; Length 101;
 Best Local Similarity 65.0%; Pred. No. 0.0096;
 Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 YGRKRRQRRKPASADGHR 20
 Db 47 YGRKRRQRRSPQDSETHQ 66

Search completed: August 24, 2006, 23:42:19
 Job time : 186 secs

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OM protein - protein search, using SW mode!

Run on: August 24, 2006, 23:37:42 ; Search time 50 Seconds
(without alignments)

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

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2: /BMC_Celerra_SID3/podata/2/iaa/6_COMBO.pep:
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4: /BMC_Celerra_SID3/podata/2/iaa/H_COMBO.pep:
5: /BMC_Celerra_SID3/podata/2/iaa/PCTUS_COMBO.pep:
6: /BMC_Celerra_SID3/podata/2/iaa/RE_COMBO.pep:
7: /BMC_Celerra_SID3/podata/2/iaa/backfile1.pep:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	73	68.2	101	2	US-10-290-579A-219	Sequence 219, App1
2	72	67.3	101	2	US-09-475-515-86	Sequence 86, App1
3	72	67.3	101	2	US-10-290-579A-223	Sequence 223, App1
4	72	67.3	101	2	US-10-290-579A-224	Sequence 224, App1
5	72	67.3	101	2	US-10-290-579A-226	Sequence 226, App1
6	72	67.3	102	2	US-09-475-515-90	Sequence 90, App1
7	71	66.4	26	1	US-09-450-257-48	Sequence 48, App1
8	71	66.4	26	1	US-08-450-246-48	Sequence 48, App1
9	71	66.4	26	1	US-08-450-098-48	Sequence 48, App1
10	71	66.4	26	1	US-08-451-233-48	Sequence 48, App1
11	71	66.4	26	1	US-08-450-236-48	Sequence 48, App1
12	71	66.4	26	1	US-08-235-403-48	Sequence 48, App1
13	71	66.4	35	1	US-08-450-257-49	Sequence 49, App1
14	71	66.4	35	1	US-08-450-246-49	Sequence 49, App1
15	71	66.4	35	1	US-08-450-098-49	Sequence 49, App1
16	71	66.4	35	1	US-08-451-233-49	Sequence 49, App1
17	71	66.4	35	1	US-08-450-236-49	Sequence 49, App1
18	71	66.4	35	1	US-08-335-403-49	Sequence 49, App1
19	71	66.4	36	1	US-08-450-257-52	Sequence 2, App1
20	71	66.4	36	1	US-08-450-246-52	Sequence 2, App1
21	71	66.4	36	1	US-08-450-098-52	Sequence 2, App1
22	71	66.4	36	1	US-08-451-233-52	Sequence 2, App1
23	71	66.4	36	1	US-08-450-236-52	Sequence 2, App1
24	71	66.4	36	2	US-09-113-921-55	Sequence 55, App1
25	71	66.4	36	2	US-08-235-403-52	Sequence 2, App1
26	66.4	36	2	US-09-336-093-56	Sequence 6, App1	

ALIGNMENTS

RESULT 1
US-10-290-579A-219
; Sequence 219, Application US/10290579A
; Patent No. 6887301
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice
; APPLICANT: Gao, Feng
; APPLICANT: Shaw, George
; TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
; FILE REFERENCE: D6287D
; CURRENT APPLICATION NUMBER: US/10/290,579A
; PRIORITY FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US/09/184,418
; PRIORITY FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 270
; SEQ ID NO 219
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: isolate=92RM009_6; genetat
; US-10-290-579A-219

Query Match 68.1%; Score 73; DB 2; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.00052; Mismatches 3; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 4;

Qy 1 YGRKIKRQRREKKPASADGHR 20
Db 47 YGRKIKRQRREKKPASSEDHQ 66

RESULT 2
US-09-475-515-86
; Sequence 86, Application US/09475515A
; Patent No. 6802705
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan
; APPLICANT: ZUR MBEGEDE, Jan
; APPLICANT: SRIVASTAVA, Indresh
; APPLICANT: LIAN, Ying
; APPLICANT: HARTOG, Karin
; APPLICANT: LIU, Hong
; APPLICANT: GREER, Catherine
; APPLICANT: SELBY, Mark
; APPLICANT: WALKER, Christopher
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
; TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES

FILE REFERENCE: 1621.002
; CURRENT APPLICATION NUMBER: US/09/475,515A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 86
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-09-475-515-86

Query Match Score 72; DB 2; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.00074; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

RESULT 3
US-10-290-579A-223
; Sequence 223, Application US/10290579A
; Patent No. 6897301
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice
; TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
; APPLICANT: Gao, Feng
; APPLICANT: Shaw, George
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS TYPE 1
; FILE REFERENCE: D6287D
; CURRENT APPLICATION NUMBER: US/10/290,579A
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 09/184,418
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 270
; SEQ ID NO: 223
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: isolate=96ZM751.3; gene=tat
; US-10-290-579A-223

Query Match Score 72; DB 2; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.00074; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

RESULT 4
US-10-290-579A-224
; Sequence 224, Application US/10290579A
; Patent No. 6897301
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice
; APPLICANT: Gao, Feng
; APPLICANT: Shaw, George
; TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
; FILE REFERENCE: D6287D
; CURRENT APPLICATION NUMBER: US/10/290,579A
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 09/184,418
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 270
; SEQ ID NO: 224
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tat cyb22

Query Match Score 72; DB 2; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.00074; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

RESULT 5
US-10-290-579A-226
; Sequence 226, Application US/10290579A
; Patent No. 6897301
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice
; APPLICANT: Gao, Feng
; APPLICANT: Shaw, George
; TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
; FILE REFERENCE: D6287D
; CURRENT APPLICATION NUMBER: US/10/290,579A
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 09/184,418
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 270
; SEQ ID NO: 226
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: isolate=94IN476.104; gene=tat
; US-10-290-579A-226

Query Match Score 67.3%; Score 72; DB 2; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.00074; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

RESULT 6
US-09-475-515-90
; Sequence 90, Application US/09475515A
; Patent No. 6602705
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: SPIVASPAVA, Indresh
; APPLICANT: LIAN, Ying
; APPLICANT: HARTOG, Karin
; APPLICANT: LIU, Hong
; APPLICANT: GREBER, Catherine
; APPLICANT: SELBY, Mark
; APPLICANT: WALKER, Christopher
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
; TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
; FILE REFERENCE: 1621.002
; CURRENT APPLICATION NUMBER: US/09/475,515A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 90
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tat cyb22

OTHER INFORMATION: SF162 protein
us-09-475-515-90

Query Match Score 72%; DB 2; Length 102;
Best Local Similarity 65.0%; Pred. No. 0.00074;
Matches 13; Conservative 3; Mismatches 4; Indels 0;
Gaps 0;

Qy 1 YGRKKRKRRRKPKASADGHR 20
Db 47 YGRKKRKRRRKPKASADGHR 66

RESULT 7
US-08-450-257-48
Sequence 48, Application US/08450257

GENERAL INFORMATION:
Patent No. 5652122

SEQUENCE: 48, Application US/08450246

APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSUM, James G.
APPLICANT: FAWELL, Stephen E.

APPLICANT: PEPINSKY, R. B.

TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,257

FILING DATE: 25-MAY-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 0/235,403

FILING DATE: 21-AUG-1992

APPLICATION NUMBER: US 07/934,375

FILING DATE: 28-APR-1994

APPLICATION NUMBER: PC-DOS/MS-DOS

FILING DATE: 25-MAY-1995

APPLICATION NUMBER: US/08/450,246

FILING DATE: 25-MAY-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/235,403

FILING DATE: 28-APR-1994

APPLICATION NUMBER: US 07/934,375

FILING DATE: 28-JUL-1993

APPLICATION NUMBER: PCT/US93/07833

FILING DATE: 19-AUG-1993

APPLICATION NUMBER: US 07/454,450

FILING DATE: 21-DEC-1992

APPLICATION NUMBER: US 07/454,450

FILING DATE: 21-DEC-1992

APPLICATION NUMBER: US 07/636,662

FILING DATE: 02-JAN-1991

APPLICATION NUMBER: US 08/158,015

FILING DATE: 24-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: B170 CIP 2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-450-257-48

Query Match Score 71; DB 1; Length 26;

Qy

1 YGRKKRKRRRKPKASADGHR 20

Best Local Similarity 65.0%; Pred. No. 0.00027;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRKRRRKPKASADGHR 20
Db 1 YGRKKRKRRRKPKASADGHR 66

RESULT 8
US-08-450-246-48
Sequence 48, Application US/08450246

Patent No. 5670617

GENERAL INFORMATION:

APPLICANT: FRANKEL, Alan

APPLICANT: PABO, Carl

APPLICANT: BARSUM, James G.

APPLICANT: FAWELL, Stephen E.

APPLICANT: PEPINSKY, R. B.

TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,246

FILING DATE: 25-MAY-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 0/235,403

FILING DATE: 21-APR-1994

APPLICATION NUMBER: US 07/934,375

FILING DATE: 21-AUG-1992

APPLICATION NUMBER: US 07/454,450

FILING DATE: 21-DEC-1992

APPLICATION NUMBER: US 07/636,662

FILING DATE: 02-JAN-1991

APPLICATION NUMBER: US 08/158,015

FILING DATE: 24-NOV-1993

APPLICATION NUMBER: US 07/454,450

FILING DATE: 21-DEC-1992

APPLICATION NUMBER: US 07/636,662

FILING DATE: 02-JAN-1991

APPLICATION NUMBER: US 08/158,015

FILING DATE: 24-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: B170 CIP 2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-450-246-48

Query Match Score 71; DB 1; Length 26;

Qy 1 YGRKKRKRRRKPKASADGHR 20

Best Local Similarity 65.0%; Pred. No. 0.00027;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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RESULT 9
US-08-450-098-48 Sequence 48, Application US/08450098
; Patent No. 5674980
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSUCCI, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINISKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESS: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.125
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,098
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1992
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hailey Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 C1P 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9090
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-450-098-48

Query Match 66.4%; Score 71; DB 1; Length 2
Best Local Similarity 65.0%; Prod. No. 0.00027; Mismatches 5; Indel
Matches 13; Conservative 2;
Qy 1 YGRKKRKRRKPKASADGHR 20
Db 1 YGRKKRKRRKPKASADGHR 20
1 YGRKKRKRRKPKASADGHR 20

```

```

RESULT 10
US-08-451-233-48 ; Sequence 48, Application US/08451233
; Patent No. 5747641 ; General Information: FRANKEL, Alan
; ; APPLICANT: PABO, Carl
; ; APPLICANT: BARSOM, James G.
; ; APPLICANT: FAWELL, Stephen E.
; ; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451.233
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-AFR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/078933
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,652
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY JR., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-451-233-48

Query Match          66.4% ; Score 71; DB 1; Length 2
Best Local Similarity 65.0% ; Prod No. 0_00027; Mismatches 5, Inde
Matches 13; Conservative 2;
Qy      1 YGRKERRQRRRKIASADGHR 20
Db      1 YGRKERRQRRRKIASADGHR 20

```

GENERAL INFORMATION:
 APPLICANT: FRANKEL, Alan
 APPLICANT: PABO, Carl
 APPLICANT: BARSOUM, James G.
 APPLICANT: FAWELL, Stephen E.
 APPLICANT: PEPINSKY, R. B.
 TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & NEAVE
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10020
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0., Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/450,236
 FILING DATE: 25-MAY-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/235,403
 FILING DATE: 28-APR-1994
 APPLICATION NUMBER: US 07/934,375
 FILING DATE: 21-AUG-1992
 APPLICATION NUMBER: US 07/098,766
 FILING DATE: 28-JUL-1993
 APPLICATION NUMBER: PCT/US93/07833
 FILING DATE: 19-AUG-1993
 APPLICATION NUMBER: US 07/934,375
 FILING DATE: 21-AUG-1992
 APPLICATION NUMBER: US 07/098,766
 FILING DATE: 28-JUL-1993
 APPLICATION NUMBER: PCT/US93/07833
 FILING DATE: 19-AUG-1993
 APPLICATION NUMBER: US 07/454,450
 FILING DATE: 21-DEC-1992
 APPLICATION NUMBER: US 07/636,662
 FILING DATE: 02-JAN-1991
 APPLICATION NUMBER: US 08/158,015
 FILING DATE: 24-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Haley Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: B170 CIP 2
 TELECOMMUNICATION INFORMATION:
 APPLICATION NUMBER: US 08/158,015
 FILING DATE: 24-NOV-1993
 TELEPHONE: (212) 596-9000
 TELEX: 14-8367
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-450-236-48

Query Match 66.4%; Score 71; DB 1; Length 26;
 Best Local Similarity 65.0%; Pred. No. 0.00027; Indels 0; Gaps 0;
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

RESULT 12
 US-08-450-235-48
 Sequence 48, Application US/08235403
 ; Patent No. 6316003
 GENERAL INFORMATION:
 APPLICANT: FRANKEL, Alan
 APPLICANT: PABO, Carl
 APPLICANT: BARSOUM, James G.
 APPLICANT: FAWELL, Stephen E.
 APPLICANT: PEPINSKY, R. B.
 TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & NEAVE

STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10020
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/450,257
 FILING DATE: 25-MAY-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/235,403
 FILING DATE: 28-APR-1994
 APPLICATION NUMBER: US 07/934,375
 FILING DATE: 21-AUG-1992
 APPLICATION NUMBER: US 07/098,766
 FILING DATE: 28-JUL-1991
 APPLICATION NUMBER: PCT/US93/07833
 FILING DATE: 19-AUG-1993
 APPLICATION NUMBER: US 07/454,450
 FILING DATE: 21-DEC-1990
 APPLICATION NUMBER: US 07/636,662
 FILING DATE: 02-JAN-1991
 APPLICATION NUMBER: US 07/454,450
 FILING DATE: 21-DEC-1990
 APPLICATION NUMBER: US 07/636,662
 FILING DATE: 02-JAN-1991
 APPLICATION NUMBER: US 08/158,015
 FILING DATE: 24-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Haley Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE DOCKET NUMBER: B170 CIP 2
 TELECOMMUNICATION INFORMATION:
 NAME: Haley Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE DOCKET NUMBER: B170 CIP 2
 TELEPHONE: (212) 596-9000
 TELEX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-450-257-49

Query Match 66.4%; Score 71; DB 1; Length 35;
 Best Local Similarity 65.0%; Pred. No. 0.00036; Mismatches 5; Indels 0; Gaps 0; Gaps 0;

Qy	1 YGRKRRQRKRKRPASADGHR 20
Db	10 YGRKRRQRKRQRPQQSQTHQ 29

RESULT 15
 US-08-450-098-49

Sequence 49, Application US/08450098
 Patent No. 5674980
 GENERAL INFORMATION:
 APPLICANT: FRANKEL, Alan
 APPLICANT: PABO, Carl
 APPLICANT: BARSUM, James G.
 APPLICANT: FAWELL, Stephen E.
 APPLICANT: PEPINSKY, R. B.
 TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & NEAVE
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA

RESULT 14
 US-08-450-246-49

Sequence 49, Application US/08450246
 Patent No. 5670617
 GENERAL INFORMATION:
 APPLICANT: FRANKEL, Alan
 APPLICANT: PABO, Carl
 APPLICANT: BARSUM, James G.
 APPLICANT: FAWELL, Stephen E.
 APPLICANT: PEPINSKY, R. B.
 TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
 NUMBER OF SEQUENCES: 69
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 CITY: New York
 STATE: New York
 COUNTRY: USA

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,098
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIORITY DATA:
PRIOR APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/635,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James P.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
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TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-450-098-49

Query Match 66.4%; Score 71; DB 1; Length 35;
Best Local Similarity 65.0%; Pred. No. 0.00036;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 1 YGRKKRRKRPASADGHR 20
Db 10 YGRKKRRKRPQQGSQTHQ 29

Search completed: August 24, 2006, 23:39:08
Job time : 51 secs

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XX Modifying N-methyl-D-aspartate receptor interaction with non-receptor
PT tyrosine kinase Src in cells, comprises administering composition
PT comprising Src-unique domains anchoring protein inhibitor to cells.

XX Claim 13; SEQ ID NO 2; 32pp; English.

XX The present invention provides a method for modifying N-methyl-D-
CC aspartate receptor (NMDAR) interaction with non-receptor tyrosine kinase
CC Src in cells. The method involves administering a composition including
CC at least one Src-unique domain anchoring protein inhibitor (SUDAPI) to
CC the cells, where modification ameliorates a disease or condition related
CC to NMDAR signaling. Diseases or conditions ameliorated by the invention
CC include stroke, hypoxia, ischemia, multiple sclerosis, Huntington's
CC chorea, Parkinson's disease, Alzheimer's disease, hyperglycemia,
CC diabetes, traumatic injury, epilepsy, grand mal seizures, spasticity,
CC cerebral palsy, asthma, cardiac arrest, macular degeneration, mental
CC diseases, schizophrenia, AIDS dementia complex, other dementias, AIDS
CC wasting syndrome, inflammation, pain, opioid addiction, cocaine addiction,
CC alcohol addiction and other conditions associated with substance abuse
CC and anorexia. The present sequence is the SUDAPI-I/HIV Tat domain fusion
CC peptide, TSUDAPI-I.

XX Sequence 20 AA;

Query Match 100.0%; Score 107; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-08; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 YGRKRRQRKRKPASADGHR 20
Db 1 YGRKRRQRKRKPASADGHR 20

RESULT 2
ADX40278 ADX40278 standard; protein; 101 AA.
XX

AC ADX40278;
DT 21-APR-2005 (first entry)

DE HIV Tat protein #20.

XX Immune stimulation; Tat.

KW Human immunodeficiency virus.

OS WO2005012502-A2.

PN 10-FEB-2005.

PD XX

PP 29-MAR-2004; 2004WO-US009510.

PR XX

DR 28-MAR-2003; 2003US-0458026P.

XX (EPIM-) EPIMMUNE INC.

XX Disclosure; Page 332-338; 458pp; English.

XX The invention relates to a method of identifying a candidate peptide
CC epitope which induces an HLA class I CTL response against variants of the
CC peptide epitope, comprising identifying, from a particular antigen of an
CC infectious agent, variants of a peptide epitope comprising primary anchor
CC residues of the same HLA class I binding motif. The method is useful for
CC identifying a candidate peptide epitope, which induces an HLA class I CTL
CC response against variants of the peptide epitope, which induces an HLA class
CC I binding motif.

XX Disclosure; Page 332-338; 458pp; English.

XX Query Match 72.9%; Score 78; DB 9; Length 100;
Best Local Similarity 70.0%; Pred. No. 0.0012; Mismatches 3; Indels 0; Gaps 0;
Matches 14; Conservative 3;

Qy 1 YGRKRRQRKRKPASADGHR 20
Db 47 YGRKRRQRKRKPASSEHQ 66

RESULT 4
ADX40367

XX The invention relates to a method of identifying a candidate peptide
CC epitope which induces an HLA class I CTL response against variants of the
CC peptide epitope, comprising identifying, from a particular antigen of an
CC infectious agent, variants of a peptide epitope comprising primary anchor

CC residues of the same HLA class I binding motif. The method is useful for
CC identifying a candidate peptide epitope, which induces an HLA class I CTL
CC response against variants of the peptide epitope. This sequence
CC represents an HIV Tat protein used in the scope of the invention.

XX Sequence 101 AA;

Query Match 74.8%; Score 80; DB 9; Length 101;
Best Local Similarity 70.0%; Pred. No. 0.00062; Mismatches 3; Indels 0; Gaps 0;
Matches 14; Conservative 3;

Qy 1 YGRKRRQRKRKPASADGHR 20
Db 47 YGRKRRQRKRKPASSEAHQ 66

RESULT 3
ADX40269 ADX40269 standard; protein; 100 AA.
ID ADX40269
XX AC ADX40269;
XX DT 21-APR-2005 (first entry)

XX DB HIV Tat protein #11.

XX KW Immune stimulation; Tat.

XX OS Human immunodeficiency virus.

XX PN WO2005012502-A2.

XX PD 10-FEB-2005.

XX PR 29-MAR-2004; 2004WO-US009510.

XX DR 28-MAR-2003; 2003US-0458026P.

XX (EPIM-) EPIMMUNE INC.

XX Disclosure; Page 332-338; 458pp; English.

XX The invention relates to a method of identifying a candidate peptide
CC epitope which induces an HLA class I CTL response against variants of the
CC peptide epitope, comprising identifying, from a particular antigen of an
CC infectious agent, variants of a peptide epitope comprising primary anchor
CC residues of the same HLA class I binding motif. The method is useful for
CC identifying a candidate peptide epitope, which induces an HLA class I CTL
CC response against variants of the peptide epitope, which induces an HLA class
CC I binding motif.

XX Disclosure; Page 332-338; 458pp; English.

XX Query Match 72.9%; Score 78; DB 9; Length 100;
Best Local Similarity 70.0%; Pred. No. 0.0012; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGRKRRQRKRKPASADGHR 20
Db 47 YGRKRRQRKRKPASSEHQ 66

XX The invention relates to an ancestral or center of tree (COT) viral
 CC nucleic acid and amino acid sequences that are determined founder
 CC sequences of highly diverse viral strain. The invention also relates to
 CC a composition comprising a highly diverse viral ancestor protein or an
 CC immunogenic fragment of an ancestor or COT protein for inducing an immune
 CC response in mammal and a method for preparing an ancestral or COT viral
 CC amino acid sequence. The composition and methods are useful for
 CC diagnosing, preventing or treating viral (e.g. HIV) infection. The
 CC invention is also useful in gene therapy. The present sequence is a clade
 CC C tat protein. This sequence is used in the comparison of the most recent
 CC common ancestor (MRCA), COT least squares (LScot) and COT minimum of
 CC means (MMCot) reconstructions for the Clade C tat gene.

XX Sequence 101 AA;

Query Match 72.9%; Score 78; DB 9; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0012; Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRKPKASADGHR 20
 Db 47 YGRKERRQRRRQRRRAPPSSSEHQ 66

RESULT 7

ADX40408 ID ADX40408 standard; protein: 101 AA.
 XX

ADX40408;
 XX

DT 21-APR-2005 (first entry)

XX HIV Tat protein #150.

XX Immune stimulation; Tat.

XX Human immunodeficiency virus.

XX WO2005012502-A2.

XX PD 10-FEB-2005.

XX 29-MAR-2004; 2004WO-US0095510.

XX PR 28-MAR-2003; 2003US-0458026P.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;

XX XY WPI; 2005-132661/14.

XX DR Disclosure; Page 333-338; 458pp; English.

XX The invention relates to a method of identifying a candidate peptide
 CC epitope which induces an HLA class I CTL response against variants of the
 CC peptide epitope, comprising identifying, from a particular antigen of an
 CC infectious agent, variants of a peptide epitope comprising primary anchor
 CC residues of the same HLA class I binding motif. The method is useful for
 CC identifying a candidate peptide epitope, which induces an HLA class I CTL
 CC response against variants of the peptide epitope. This sequence
 XX represents an HIV Tat protein used in the scope of the invention.

SQ Sequence 101 AA;

Query Match 72.0%; Score 77; DB 9; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0017; Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRKPKASADGHR 20
 Db 47 YGRKERRQRRRQRRSAPASSEDHQ 66

RESULT 9

AAR10515 ID AAR10515 standard; protein: 72 AA.
 XX

AC AAR10515;

XX DT 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 04-APR-1991 (first entry)

DE ARV tat gene product.

XX Sequence 101 AA;
 SQ Query Match 72.0%; Score 77; DB 9; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0017;

XX Human T-cell leukaemia virus; HTLV-III; acquired immune deficiency; AIDS;
 KW transactivation; LAV.
 XX Human immunodeficiency virus.
 OS US4981790-A.
 PN 01-JAN-1991.
 PD 06-DEC-1985; 85US-00806263.
 PR 25-MAY-1984; 84US-00614297.
 XX PA (DAND) DANA FARRER CANCER INST INC.
 XX PS Disclosure: Fig 7; 16pp; English.
 XX The sequence is that of the tatIII gene product, which regulates gene
 CC expression directed by the HTLV-III/LPV long terminal repeat. See also
 CC AAR10511-14. (Updated on 10-MAR-2003 to add missing OS field.) (Updated
 CC on 20-MAR-2003 to correct PA field.)
 XX SQ Sequence 72 AA;
 Query Match 70.1%; Score 75; DB 2; Length 72;
 Best Local Similarity 70.0%; Pred. No. 0.0024; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 XX Qy 1 YGRKKRQRRRKPSADGHR 20
 Db 47 YGRKKRQRRRKPSADGHR 66

RESULT 10
 ADX40365 ID ADX40365 standard; protein: 100 AA.
 AC ADX40365;
 XX DT 21-APR-2005 (first entry)
 XX DE HIV Tat protein #107.
 XX KW Immune stimulation; Tat.
 XX OS Human immunodeficiency virus.
 PN WO2005012502-A2.

Query Match 70.1%; Score 75; DB 2; Length 72;
 Best Local Similarity 70.0%; Pred. No. 0.0024; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 XX Qy 1 YGRKKRQRRRKPSADGHR 20
 Db 47 YGRKKRQRRRKPSADGHR 66

RESULT 11
 ADX40316 ID ADX40316 standard; protein: 101 AA.
 AC ADX40316;
 XX DT 21-APR-2005 (first entry)
 XX DE HIV Tat protein #58.
 XX KW Immune stimulation; Tat.
 XX OS Human immunodeficiency virus.
 PN WO200501252-A2.
 XX PD 10-FEB-2005.
 XX PF 29-MAR-2004; 2004WO-US009510.
 XX PR 28-MAR-2003; 2003US-0458026P.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;
 XX DR WPI; 2005-132661/14.
 XX PS Disclosure: Page 333-339; 458pp; English.

XX The invention relates to a method of identifying a candidate peptide
 CC epitope which induces an HLA class I CTL response against variants of the
 CC peptide epitope, comprising identifying, from a particular antigen of an
 CC infectious agent, variants of a peptide epitope comprising primary anchor
 CC residues of the same HLA class I binding motif. The method is useful for
 CC identifying a candidate peptide epitope, which induces an HLA Class I CTL
 CC response against variants of the peptide epitope. This sequence
 CC represents an HIV Tat protein used in the scope of the invention.
 XX SQ Sequence 101 AA;
 Query Match 70.1%; Score 75; DB 9; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0033; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 4;

XX Identifying a candidate peptide epitope, which induces a HLA class I CTL
 PR response comprises identifying variants of a peptide epitope 8-11 amino
 PR acids in length comprising primary anchor residues of the same HLA class

Qy	1 YGRKKRQRRRKPSADGHR 20 47 YGRKKRQRRRKPSADGHR 66	OS Human immunodeficiency virus. XX WO2005012502-A2.
Db		XX PD 10-FEB-2005. XX PF 29-MAR-2004; 2004WO-US009510. XX PR 28-MAR-2003; 2003US-0458026P. XX PA (EPIM-) EPIMMUNE INC.
RESULT 12 ADX40407 ID ADX40407 standard; protein: 101 AA. XX AC AC0407; DT 21-APR-2005 (first entry) XX DB HIV Tat protein #149. XX KW Immune stimulation; Tat. XX OS Human immunodeficiency virus. XX PN WO2005012502-A2. XX PR 10-FEB-2005. XX PF 29-MAR-2004; 2004WO-US009510. XX PR 28-MAR-2003; 2003US-0458026P. XX PA (EPIM-) EPIMMUNE INC. XX PI Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ; XX WPI; 2005-132661/14. XX PS Disclosure; Page 333-339; 458pp; English.	XX The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope, comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HIV Tat protein used in the scope of the invention. XX SQ Sequence 101 AA: XX Query Match 70.1%; Score 75; DB 9; Length 101; Best Local Similarity 70.0%; Pred. No. 0.0033; Indels 0; Mismatches 2; Gap 0; Matches 14; Conservative 4; Delins 0; Gaps 0; XX Qy 1 YGRKKRQRRRKPSADGHR 20 Db 47 YGRKKRQRRRKPSADGHR 66	
Qy	1 YGRKKRQRRRKPSADGHR 20 47 YGRKKRQRRRKPSADGHR 66	RESULT 14 ADX40285 standard; protein: 102 AA. XX AC AC0285; DT 21-APR-2005 (first entry) XX DB HIV Tat protein #27. XX KW Immune stimulation; Tat. XX OS Human immunodeficiency virus. XX PN WO2005012502-A2. XX PR 10-FEB-2005. XX PF 29-MAR-2004; 2004WO-US009510. XX PA (EPIM-) EPIMMUNE INC.
Db		XX The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope, comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HIV Tat protein used in the scope of the invention. XX SQ Sequence 101 AA: XX Query Match 70.1%; Score 75; DB 9; Length 101; Best Local Similarity 70.0%; Pred. No. 0.0033; Indels 0; Mismatches 2; Gap 0; Matches 14; Conservative 4; Delins 0; Gaps 0; XX Qy 1 YGRKKRQRRRKPSADGHR 20 Db 47 YGRKKRQRRRKPSADGHR 66
RESULT 13 ADX0319 ID ADX0319 standard; protein: 101 AA. XX AC ADX0319; DT 21-APR-2005 (first entry) XX DB HIV Tat protein #61. XX KW Immune stimulation; Tat. XX PR 28-MAR-2003; 2003US-0458026P. XX PA (EPIM-) EPIMMUNE INC.	XX The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of a peptide epitope, comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HIV Tat protein used in the scope of the invention. XX SQ Sequence 101 AA: XX Query Match 70.1%; Score 75; DB 9; Length 101; Best Local Similarity 70.0%; Pred. No. 0.0033; Indels 0; Mismatches 2; Gap 0; Matches 14; Conservative 4; Delins 0; Gaps 0; XX Qy 1 YGRKKRQRRRKPSADGHR 20 Db 47 YGRKKRQRRRKPSADGHR 66	

PR acids in length comprising primary anchor residues of the same HLA class I binding motif.
 PR Disclosure: Page 333-338; 458pp; English.
 XX

CC The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the infectious agent, comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HIV Tat protein used in the scope of the invention.

XX Sequence 102 AA;

Query Match Score 75; DB 9; Length 102;
 Best Local Similarity 65.0%; Pred. No. 0.0034; Gaps 0;
 Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGRKKRKRRRKPAASADGHR 20
 Db 47 YGRKKRKRRRSAPSSSENHQ 66

RESULT 15

AAU84590 standard; protein; 1896 AA.

AAU84590;

AC

XX

DT

08-MAY-2002 (first entry)

XX

DE

HIV Cassette A1 Protein.

XX

KW

Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;

KW

viral infection; human immunodeficiency virus; melanoma;

KW

bacterial infection; Salmonella; Legionella; parasitic infection;

KW

Trypanosoma; Toxoplasma; Giardia.

XX

OS Human immunodeficiency virus 1.

OS Syntheic.

XX

PN WO20010197-A1.

XX

PD 29-NOV-2001.

XX

PP 25-MAY-2001; 2001WO-AU000622.

XX

PR 26-MAY-2000; 2000AU-00007761.

XX

PA (AUSU) UNIV AUSTRALIAN NAT.

XX

PI Thomson SA, Ramshaw IA;

XX

DR WPI: 2002-147575/19.

DR N-PSDB, ABK36429.

XX

PR New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a pathogen or cancer.

XX

PS Example 1; SEQ ID NO 393; 364pp; English.

XX

CC The invention relates to new synthetic polypeptide (I) comprising

CC several different segments of at least one parent polypeptide linked

CC together in a different relationship relative to their linkage in the

CC parent polypeptide to impede, abrogate or otherwise alter at least one

CC function associated with the parent polypeptide and for inducing an

CC immune response against a pathogen or cancer. Also included are a

CC synthetic polynucleotide encoding and computer system for designing the

CC synthetic polypeptides. The synthetic polypeptides and polynucleotides

CC are referred to as a Savine. The synthetic polypeptide is useful for
 CC modulating immune responses preferably directed against a pathogen or a
 CC cancer. (e.g., cancers of the lung, breast, ovary, cervix, colon, head
 CC and neck, pancreas, prostate, bladder, kidney, bone liver,
 CC oesophagus, brain, testicle, uterus, as potentiating agents.
 CC Compositions comprising the polypeptide may be used in the treatment or
 CC prophylaxis against viral (such as infections caused by HIV (human
 CC immunodeficiency virus), hepatitis, Japanese encephalitis
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
 CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
 CC a cassette protein consisting of several peptides derived from a parent
 CC protein. One or more cassettes are used to construct a savine of the
 CC invention

XX Sequence 1896 AA;

SQ

Query	1 YGRKKRKRRRKPAASADGHR 20
Match	186 YGRKKRKRRRKPAASADGHR 205
Best	Score 75; Pred. No. 0.05;
Local	Length 1896;
Similarity	70.1%; Mismatches 4; Indels 0; Gaps 0;
Matches	14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy	1 YGRKKRKRRRKPAASADGHR 20
Db	186 YGRKKRKRRRKPAASADGHR 205

XX Search completed: August 24, 2006, 23:32:23
 Job time : 198 secs

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